
WATERMAN

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:16:02 1998: Maspar time 0.08 seconds
422.695 Million cell updates/sec
Tabular output not generated.

Title: >US-08-844-215-7
Description: (1-125) from US08844215 pep
Perfect Score: 949
Sequence: 1 EVOLLESGSEVKKPGSSVKV

..... GSCWGWFDPWGGLTVTVSS 126

Scoring table: PAM 150
Gap 11

Searched: 95051 seqs, 30469580 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r53
1:ann1 2:ann2 3:ann3 4:ann4 5:ann5 6:ann6 7:ann7
8:ann8 9:ann9 10:ann10 11:ann11 12:ann12 13:ann13
14:ann14 15:ann15 16:ann16 17:ann17 18:unrev

Statistics: Mean 40.893; Variance 107.589; scale 0.380

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	754	79.5	125	7	PH0957 Ig heavy chain V reg	4.99e-96	
2	671	70.7	128	3	PH0952 Ig heavy chain V reg	4.62e-83	
3	661	69.7	129	7	A33548 Ig heavy chain V-1 r	1.66e-81	
4	657	69.2	116	7	PH0959 Ig heavy chain V reg	6.97e-81	
5	648	68.3	132	7	PH0958 Ig heavy chain V reg	1.75e-79	
6	646	68.1	120	7	PH0962 Ig heavy chain V reg	3.57e-79	
7	642	67.7	126	7	B33548 Ig heavy chain V-1 r	1.49e-78	
8	642	67.7	127	7	PH0955 Ig heavy chain V reg	1.49e-78	
9	639	67.3	132	7	PH0454 Ig heavy chain V reg	4.37e-78	
10	638	67.2	119	7	PH0961 Ig heavy chain V reg	6.24e-78	
11	634	66.8	121	7	A49590 Ig heavy chain V reg	2.61e-77	
12	633	66.7	135	7	PH0953 Ig heavy chain V reg	3.72e-77	
13	632	66.6	133	7	C33548 Ig heavy chain V-1 r	5.32e-77	
14	632	66.6	627	7	S14583 Ig mu chain precursor	5.32e-77	
15	629	66.3	98	7	S26913 Ig heavy chain V reg	1.55e-76	
16	629	66.3	116	7	S31698 Ig heavy chain precursor	1.55e-76	
17	629	66.3	123	7	S4108 Ig heavy chain V-1 r	1.55e-76	
18	628	66.2	116	7	S26261 Ig heavy chain V reg	2.22e-76	
19	627	66.1	198	7	S24580 Ig heavy chain V-1 r	3.17e-76	
20	622	65.5	136	7	PH0960 Ig heavy chain V reg	1.89e-75	

21	620	55.3	132	7	S46394 Ig heavy chain V reg	3.86e-75
22	619	55.2	119	7	S44106 Ig heavy chain V-D-J	5.51e-75
23	616	64.9	113	7	PH1663 Ig heavy chain V reg	1.61e-74
24	595	62.7	98	7	S46463 Ig heavy chain V-1 r	2.85e-71
25	592	62.4	135	7	B32274 Ig heavy chain precursor	8.28e-71
26	591	62.3	117	2	G1H0EU Ig heavy chain V-1 r	1.18e-70
27	591	62.3	122	7	B49590 Ig heavy chain V reg	1.18e-70
28	585	61.6	122	7	C49590 Ig heavy chain V reg	9.97e-70
29	584	61.5	97	7	PH0870 Ig heavy chain V reg	1.42e-69
30	581	61.2	150	7	PL0105 anti-PR2 erythrocyte	4.13e-69
31	578	60.9	116	7	S31667 Ig heavy chain V reg	1.20e-68
32	572	60.3	98	7	A20523 Ig heavy chain V-1 r	1.01e-67
33	567	59.7	108	7	PH1664 Ig heavy chain V reg	5.94e-67
34	567	59.7	123	7	D33548 Ig heavy chain V-1 r	5.94e-67
35	559	58.9	124	7	S19665 Ig heavy chain V reg	1.01e-65
36	557	58.7	129	7	S36260 Ig heavy chain V reg	2.05e-65
37	556	58.6	136	7	I44151 Ig heavy chain V reg	2.93e-65
38	555	58.5	109	7	PH1671 Ig heavy chain V reg	4.17e-65
39	554	58.4	171	7	S23623 Ig heavy chain V reg	5.94e-65
40	545	57.5	148	7	S23257 Ig heavy chain V reg	1.01e-63
41	545	57.4	122	7	S36271 Ig heavy chain V reg	1.43e-63
42	539	56.8	127	7	S34014 Ig heavy chain V reg	1.19e-62
43	539	56.8	142	7	A32483 Ig heavy chain V reg	1.19e-62
44	538	56.7	129	7	S46393 Ig heavy chain V reg	1.70e-62
45	536	56.5	118	7	S36265 Ig heavy chain V reg	3.45e-62

ALIGNMENTS

RESULT 1
ENTRY PH0957 #type fragment
TITLE Ig heavy chain V region (G6+ CIL-BRA) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
ACCESSION PH0957
REFERENCE PH0952
#authors Martin, I., Duff, S.F., Barsby, D.A., Kuffs, J.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92302880
#accession PH0957
##status nucleic acid sequence not shown
##molecule_type DNA
##residues 1-125 ##label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
FEATURE
1-30
15-98
31-35
36-50
51-67
68-98
99-113
SUMMARY
#region framework 1\
#domain immunoglobulin homology #label IMM\
#region complementarity-determining 1\
#region framework 2\
#region complementarity-determining 2\
#region framework 3\
#region complementarity-determining 3
#length 125 #checksum 8143

Query Match 79.5% Score 754, DB 7, Length 125,
Best Local Similarity 83.8%; Pred No, 4.99e-96;
Matches 107; Conservative 9; Mismatches 7; Indels 5; Gaps 3;
Db 1 gqqlvsggavkpgssvkysckasgttssvaimwrrgpggggagwggilpigtany 60
|||||
QY 1 EVOLLESGSEVKKPGSSVKVSCPASGGSFSPSYFNWVRQAPGQGLEWMGSIIPMFGTANY 60
Db 61 aqkfqrvttadestntaymelslrsdtaavyocard-g--csggscyfwgfdpwwgq 117
|||||
QY 61 AQKFGQFVTTTADESTATGYMELSLPSETAVYVCAMPYPKHCSRGS--WGWFDPWQ 118
Db 118 gtlvtvss 125
QY 119 GTLVTVSS 126

```

RESULT      2
ENTRY       PH0952      #type fragment
TITLE       Ig heavy chain V region (G6+ CLL-SM1) - human (fragment)
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        17-Apr-1993 #sequence_revision 17-Apr-1993 #ext_change
            16-Aug-1996
ACCESSIONS  PH0952
REFERENCE    Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#authors    J. Exp. Med. (1992) 175:983-991
#journal     Evidence for somatic selection of natural autoantibodies
#title       cross-references MUID:92202880
#accession  PH0952      nucleic acid sequence not shown
#status      ##molecule_type DNA
#residues    1-128 ##label MAR
CLASSIFICATION
KEYWORDS     #superfamily immunoglobulin V region: immunoglobulin homology
             heterotetramer: immunoglobulin
FEATURE      1-30      #region framework 1\
             15-98      #domain immunoglobulin homology #label IMM\
             31-35      #region complementarity-determining 1\
             36-50      #region framework 2\
             51-67      #region complementarity-determining 2\
             68-98      #region framework 3\
             99-116     #region complementarity-determining 3\
SUMMARY      #length 128 #molecular_weight 13432 #checksum 4075

Query Match      70.7%; Score 671; DB 7; Length 128;
Best Local Similarity 75.8%; Pred. No. 4.62e-83;
Matches          97; Conservative 15; Mismatches 14; Indels 2; Gaps 1;

Db      1 qvqlvqgaevkpkpssvksskqstfssyaiswrrqapqqlwmgqilpftany 60
Qy      1 EVQLLESGSEVKPKGSVKVSCRASGSGSPSYNFNWWVPQAPGSGLEWMGGIIPMEGTANY 60
Db      61 aqkfgqrvtitadeststymelsslrdsedavvyqargnydiwgsyrsndafdiwq 120
Qy      61 AQKFGQGRVTITADESTATGYMELSSLSRSEDATVAVYQAMPYPKHCSPGSGW--FNPWGQ 118
Db      121 gtmvtvss 128
Qy      119 GTLVTVSS 126

RESULT      3
ENTRY       A33548      #type complete
TITLE       Ig heavy chain V-1 region (NE1) - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        17-Jan-1990 #sequence_revision 17-Jan-1990 #ext_change
            16-Aug-1996
ACCESSIONS  A33548; PH0956
REFERENCE    Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.F.;
             Carson, D.A.
#authors     Proc Natl Acad Sci U S A (1990) 86:5913-5917
#journal     Developmentally restricted immunoglobulin heavy chain
#title       variable region gene expressed at high frequency in chronic
             lymphocytic leukemia.
#cross-references MUID:89345575
#accession  A33548      preliminary: not compared with conceptual translation
#status      ##molecule_type mRNA
#residues    1-129 ##label KIP
REFERENCE    PH0952
#authors     Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal     J. Exp. Med. (1992) 175:983-991
#title       Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
#accession  PH0956      nucleic acid sequence not shown
#status      ##molecule_type DNA

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##residues    1-129 ##label MAR
CLASSIFICATION
KEYWORDS     #superfamily immunoglobulin V region: immunoglobulin homology
             heterotetramer: immunoglobulin
FEATURE      1-30      #region framework 1\
             15-98      #domain immunoglobulin homology #label IMM\
             31-35      #region complementarity-determining 1\
             36-50      #region framework 2\
             51-67      #region complementarity-determining 2\
             68-98      #region framework 3\
             99-117     #region complementarity-determining 3\
SUMMARY      #length 129 #molecular_weight 13432 #checksum 4075

Query Match      69.7%; Score 661; DB 7; Length 129;
Best Local Similarity 76.9%; Pred. No. 1.66e-81;
Matches        100; Conservative 13; Mismatches 12; Indels 5; Gaps 4;

Db      1 qvqlvqgaevkpkpssvksskqstfssyaiswrrqapqqlwmgqilpftany 60
Qy      1 EVQLLESGSEVKPKGSVKVSCRASGSGSPSYNFNWWVPQAPGSGLEWMGGIIPMEGTANY 60
Db      61 aqkfgqrvtitadeststymelsslrdsedavvyqargnydiwgsyrsndafdiwq 119
Qy      61 AQKFGQGRVTITADESTATGYMELSSLSRSEDATVAVYQAMPYPKHCSPGSGW--FNPWGQ 116
Db      120 gtmvtvss 129
Qy      117 GTLVTVSS 126

RESULT      4
ENTRY       PH0959      #type fragment
TITLE       Ig heavy chain V region (G6+ T-L26) - human (fragment)
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        17-Apr-1993 #sequence_revision 17-Apr-1993 #ext_change
            16-Aug-1996
ACCESSIONS  PH0959
REFERENCE    Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#authors     J. Exp. Med. (1992) 175:983-991
#journal     Evidence for somatic selection of natural autoantibodies.
#title       cross-references MUID:92202880
#accession  PH0959      nucleic acid sequence not shown
#status      ##molecule_type DNA
#residues    1-116 ##label MAR
CLASSIFICATION
KEYWORDS     #superfamily immunoglobulin V region: immunoglobulin homology
             heterotetramer: immunoglobulin
FEATURE      1-30      #region framework 1\
             15-98      #domain immunoglobulin homology #label IMM\
             31-35      #region complementarity-determining 1\
             36-50      #region framework 2\
             51-67      #region complementarity-determining 2\
             68-98      #region framework 3\
             99-104     #region complementarity-determining 3\
SUMMARY      #length 116 #checksum 5596

Query Match      69.2%; Score 657; DB 7; Length 116;
Best Local Similarity 80.2%; Pred. No. 6.97e-81;
Matches        101; Conservative 11; Mismatches 4; Indels 10; Gaps 2;

Db      1 qvqlvqgaevkpkpssvksskqstfssyaiswrrqapqqlwmgqilpftany 60
Qy      1 EVQLLESGSEVKPKGSVKVSCRASGSGSPSYNFNWWVPQAPGSGLEWMGGIIPMEGTANY 60
Db      61 aqkfgqrvtitadeststymelsslrdsedavvyqargnydiwgsyrsndafdiwq 110
Qy      61 AQKFGQGRVTITADESTATGYMELSSLSRSEDATVAVYQAMPYPKHCSPGSGW--FNPWGQ 120
Db      111 lvtvss 116
Qy      121 LVTVSS 126

```



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#journal      J. Exp. Med. (1992) 175:983-991
#title        Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
#accession    PH0955
##status      nucleic acid sequence not shown
##molecule_type DNA
##residues     1-127 ##label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE
1-30           #region framework 1\
15-98          #domain immunoglobulin homology #label IMM\
31-35          #region complementarity-determining 1\
36-50          #region framework 2\
51-67          #region complementarity-determining 2\
68-98          #region framework 3\
99-115         #region complementarity-determining 3
SUMMARY        #length 127 #checksum 6297

Query Match      67.7%; Score 642; DB 7; Length 127;
Best Local Similarity 74.0%; Pred. No. 1.49e-78;
Matches 94; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

Db 1 qqlvsgaevkpkssvkvscasggtfssyaiswvraqpgqglewmggilpifgtany 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1 EVOLLESSEVKKPGSSVKVSCFASGSGSPSYNFWVPQAPCGGLEWVGSIIPMGFTANY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 61 akkfgrvritadeststymelssrdsdtavvyrcarvsifgvvqhyyvymdvwkg 120
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 AKKFGGRVITADESTATGYMELSSRSEDATVYYVCAMPYKPKHCSFGSCWGF-DPMFGQ 119
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 121 tvtvss 127
1-111
QY 120 TLTVSS 126

RESULT 9
ENTRY      PH0954
TITLE      Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
ACCESSIONS PH0954
#authors    Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal    J. Exp. Med. (1992) 175:983-991
#title      Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
#accession  PH0954
##status     nucleic acid sequence not shown
##molecule_type DNA
##residues   1-132 ##label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE
1-30           #region framework 1\
15-98          #domain immunoglobulin homology #label IMM\
31-35          #region complementarity-determining 1\
36-50          #region framework 2\
51-67          #region complementarity-determining 2\
68-98          #region framework 3\
99-120         #region complementarity-determining 3
SUMMARY        #length 132 #checksum 9232

Query Match      67.7%; Score 639; DB 7; Length 132;
Best Local Similarity 72.7%; Pred. No. 4.37e-78;
Matches 96; Conservative 16; Mismatches 14; Indels 6; Gaps 3;

Db 1 qqlvsgaevkpkssvkvscasggtfssyaiswvraqpgqglewmggilpifgtany 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1 EVOLLESSEVKKPGSSVKVSCFASGSGSPSYNFWVPQAPCGGLEWVGSIIPMGFTANY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 61 akkfgrvritadeststymelssrdsdtavvyrcarphasiddfwsgyyfnvyygm 120

```

```

||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 AKKFGGRVITADESTATGYMELSSRSEDATVYYVCAMPYKPKHCSFGSCWGF-DPMFGQ 114
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 121 vdgqgttvtvss 132
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 115 PWGGGLTVTVSS 126

RESULT 10
ENTRY      PH0961
TITLE      Ig heavy chain V region (G6+ T-L33) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
ACCESSIONS PH0961
#authors    Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal    J. Exp. Med. (1992) 175:983-991
#title      Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
#accession  PH0961
##status     nucleic acid sequence not shown
##molecule_type DNA
##residues   1-119 ##label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE
1-30           #region framework 1\
15-98          #domain immunoglobulin homology #label IMM\
31-35          #region complementarity-determining 1\
36-50          #region framework 2\
51-67          #region complementarity-determining 2\
68-98          #region framework 3\
99-107         #region complementarity-determining 3
SUMMARY        #length 119 #checksum 8601

Query Match      67.2%; Score 638; DB 7; Length 119;
Best Local Similarity 85.0%; Pred. No. 6.24e-78;
Matches 85; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Db 1 qqlvsgaevkpkssvkvscasggtfssyaiswvraqpgqglewmggilpifgtany 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1 EVOLLESSEVKKPGSSVKVSCFASGSGSPSYNFWVPQAPCGGLEWVGSIIPMGFTANY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 61 akkfgrvritadeststymelssrdsdtavvyrcarg 100
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 AKKFGGRVITADESTATGYMELSSRSEDATVYYVCAMPY 100
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 11
ENTRY      A49590
TITLE      Ig heavy chain V region (ACHSV1, clone 15) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
23-May-1997
ACCESSIONS A49590
#authors    Burioni, R.; Williamson, R.A.; Sanna, P.P.; Bloom, F.E.;
            Burton, D.R.
#journal    Proc. Natl. Acad. Sci. U S A (1994) 91:355-359
#title      Recombinant human Fab to glycoprotein B neutralizes
            infectivity and prevents cell-to-cell transmission of
            herpes simplex viruses 1 and 2 in vitro.
#cross-references MUID:94105168
#accession  A49590
##status     preliminary, not compared with conceptual translation
##molecule_type nucleic acid
##residues   1-121 ##label BUR
##cross-references NCBI:141850
##experimental_source bone marrow lymphocytes
##note       sequence extracted from NCBI backbone
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin
KEYWORDS       heterotetramer; immunoglobulin

```


[illegible]

QY 114 DPWGGTILVTVSS 126

```

RESULT 15
ENTRY S26915 #type fragment
TITLE Ig heavy chain V region (DP-10) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
06-Jun-1997
ACCESSIONS S26915
REFERENCE S26885
#authors Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.;
Winter, G.
#journal J. Mol. Biol. (1992) 227:776-798
#title The repertoire of human germline V(H) sequences reveals about
fifty groups of V(H) segments with different hypervariable
loops.
#accession S26915
##status preliminary
##molecule_type DNA
##residues 1-98 ##label TOM
##cross-references EMBL:Z12312
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
13-98 #domain immunoglobulin homology #label IMM
SUMMARY
length 98 #checksum 3310

Query Match 66.3%; Score 629; DB 7; Length 98;
Rest Local Similarity 86.6%; Pred. No. 1.55e-76;
Matches 84; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

Db 1 qvqlvqsgaevkpkgsykvskcasqgtfssyaiswvrqapggqlwmqgiipifqtany 60
QY 1 EYQLLESGEVKKPGSSVKVSCPASGGSPFPYFNFWPQAPGQGLEWMGGIIPMEGTANY 60

Db 61 aqkfggrvtitadeststaymelslrsedtavyyca 97
QY 61 AQKFGGRVTITADESTATGYMELSLRSEDTAVYYCA 97

```

Search completed: Tue Feb 24 07:16:18 1998
Job time : 16 secs.

WQRELE (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:42:43 1998; Maspar time 3.28 Seconds
Tabular output not generated. 195,669 Million cell updates/sec

Title: >US-08-844-215-7
Description: (1-126) from US08844215.pep
Perfect Score: 949
Sequence: 1 EVOLLESGSEVKKPGSSVKV ... GSGWGFDPWGGGTLTVTS 126

Scoring table: PAM 150
Gap 11

Searched: 56402 seqs, 5095871 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:back1 2.51 3.52 4 53 5 54 6 55 7 56 8:PCR90 9 PCR31
10:PCR92 11:PCR93 12:PCR94 13:PCR95 14:PCR96

Statistics: Mean 28.440; Variance 143 456; scale 0 198

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	635	66.9	120	11	PCT-US93-1 Sequence 13, Applicati	1.04e-42
2	609	64.2	120	11	PCT-US93-1 Sequence 12, Applicati	1.48e-40
3	605	63.8	129	13	PCT-US95-0 Sequence 45, Applicati	3.18e-40
4	604	63.6	147	6	US-08-217 Sequence 4, Applicati	3.85e-40
5	595	62.7	102	10	PCT-US92-0 Sequence 55, Applicati	2.14e-39
6	595	62.7	102	7	US-08-053 Sequence 63, Applicati	2.14e-39
7	595	62.7	102	10	PCT-US92-1 Sequence 63, Applicati	2.14e-39
8	595	62.7	102	7	US-07-834 Sequence 55, Applicati	2.14e-39
9	591	62.3	117	6	US-08-474 Sequence 15, Applicati	4.58e-39
10	591	62.3	117	6	US-08-477 Sequence 104, Applicati	4.58e-39
11	591	62.3	117	6	US-08-477 Sequence 4, Applicati	4.58e-39
12	591	62.3	117	6	US-08-477 Sequence 15, Applicati	4.58e-39
13	591	62.3	117	6	US-08-477 Sequence 72, Applicati	4.58e-39
14	591	62.3	117	6	US-07-634 Sequence 15, Applicati	4.58e-39
15	591	62.3	117	6	US-07-634 Sequence 4, Applicati	4.58e-39
16	591	62.3	117	6	US-07-634 Sequence 72, Applicati	4.58e-39
17	591	62.3	117	6	US-07-634 Sequence 104, Applicati	4.58e-39
18	591	62.3	117	7	US-08-474 Sequence 4, Applicati	4.58e-39
19	591	62.3	117	7	US-08-487 Sequence 15, Applicati	4.58e-39
20	591	62.3	117	7	US-08-487 Sequence 72, Applicati	4.58e-39
21	591	62.3	117	7	US-08-474 Sequence 104, Applicati	4.58e-39
22	591	62.3	117	7	US-08-474 Sequence 72, Applicati	4.58e-39

23	591	62.3	117	7	US-08-487-Sequence 4, Applicatio	4.58e-39
24	591	62.3	117	7	US-08-487-Sequence 104, Applicat	4.58e-39
25	587	61.9	122	13	PCT-US95-0 Sequence 2, Applicatio	9.82e-39
26	553	58.3	98	6	US-08-211-Sequence 140, Applicat	6.31e-36
27	553	58.3	128	7	US-08-478-Sequence 63, Applicati	6.31e-36
28	545	57.4	140	11	PCT-US93-1 Sequence 12, Applicati	2.88e-35
29	540	56.9	119	13	PCT-US95-0 Sequence 12, Applicati	7.45e-35
30	536	56.5	121	11	PCT-US93-1 Sequence 8, Applicatio	1.59e-34
31	532	56.1	97	14	PCT-US96-0 Sequence 16, Applicati	3.40e-34
32	531	56.0	116	7	US-08-487-Sequence 6, Applicatio	4.11e-34
33	531	56.0	116	6	US-08-477-Sequence 6, Applicatio	4.11e-34
34	531	56.0	116	6	US-07-634-Sequence 6, Applicatio	4.11e-34
35	531	56.0	116	7	US-08-474-Sequence 6, Applicatio	4.11e-34
36	526	55.4	121	6	US-07-634-Sequence 53, Applicati	1.06e-33
37	526	55.4	121	7	US-08-487-Sequence 53, Applicati	1.06e-33
38	526	55.4	121	6	US-08-477-Sequence 53, Applicati	1.06e-33
39	526	55.4	121	7	US-08-474-Sequence 53, Applicati	1.06e-33
40	524	55.2	119	13	PCT-US95-0 Sequence 10, Applicati	1.55e-33
41	523	55.1	123	13	PCT-US95-0 Sequence 11, Applicati	1.87e-33
42	523	55.1	142	13	PCT-US95-0 Sequence 17, Applicati	1.87e-33
43	522	55.0	119	13	PCT-US95-0 Sequence 13, Applicati	2.26e-33
44	519	54.7	140	6	US-07-946-Sequence 28, Applicati	3.99e-33
45	518	54.6	97	13	PCT-US95-1 Sequence 13, Applicati	4.82e-33

ALIGNMENTS

RESULT	1	STANDARD:	PPT:	120 AA.
ID	PCT-US93-10555-13			
XX	xxxxxx			
AC	xxxxxx			
XX	01-JAN-1900			
DT				
XX	Sequence 13, Application PC/TUS9310555.			
DE				
XX	Sequence 13, Application PC/TUS9310555			
CC	GENERAL INFORMATION			
CC	APPLICANT: SILVERMAN, GREGG J.			
CC	TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF			
CC	TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES			
CC	THROUGH			
CC	TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG			
CC	ATES			
CC	TITLE OF INVENTION: THEREOF			
CC	NUMBER OF SEQUENCES: 51			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESSEE: Spensley Horn Jubas & Lubitz			
CC	STREET: 1800 Century Park East - Suite 500			
CC	CITY: Los Angeles			
CC	STATE: California			
CC	COUNTRY: USA			
CC	ZIP: 90067			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC	COMPUTER: IBM PC compatible			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	SOFTWARE: Patent Release #1.0, Version #1.25			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: PCT/US93/10555			
CC	FILING DATE: 29-OCT-1993			
CC	CLASSIFICATION:			
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: Howells, Stacy L.			
CC	REGISTRATION NUMBER: 34,842			
CC	REFERENCE/DOCKET NUMBER: PD-2630			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: (619) 455-5100			
CC	TELEFAX: (619) 455-5110			
CC	INFORMATION FOR SEQ ID NO: 13:			
CC	SEQUENCE CHARACTERISTICS:			
CC	LENGTH: 120 amino acids			
CC	TYPE: amino acid			

CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: KAS
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..120
SQ SEQUENCE 120 AA: 13008 MW: 78865 CN:

Query Match 66 %; Score 635; DB 11; Length 120;
Best Local Similarity 73.8%; Pred. No. 1.04e-42;
Matches 93; Conservative 15; Mismatches 11; Indels 7; Gaps 6;
Db 1 VHLVQSGAEVKPGSSVKYSCKASGTFSSYAISWVP-APQASIFEMSGSIPIPIFQANYA 60
QY 2 VOLLESGSEVKPGSSVKYSCKASGTFSSYFNFNWVPQAPQQLKWMQSIIPMFQIANYA 61
Db 61 QKFGQVTTITADESTNTATMELRLSRLSDTAMYYCAKESYGDY-CP-P-FLD-F--WQGGT 114
QY 62 QKFGQVTTITADESTNTATMELRLSRLSDTAMYYCAKESYGDY-CP-P-FLD-F--WQGGT 114
Db 115 LVTSS 120
QY 121 LVTSS 126

RESULT 2
ID PCT-US93-10555-12 STANDARD: PRT: 120 AA.

XX XXXXXX
AC XXXXXX
DT 01-JAN-1900

DE Sequence 12, Application PC/TUS93/10555
XX Sequence 12, Application PC/TUS93/10555
CC GENERAL INFORMATION:
CC APPLICANT: SILVERMAN, GREGG J.
CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
CC THROUGH
CC ATES
CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG

CC TITLE OF INVENTION: THEREOF
CC NUMBER OF SEQUENCES: 51
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Jubas & Lubitz
CC STREET: 1880 Century Park East - Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/10555
CC FILING DATE: 29-OCT-1993
CC CLASSIFICATION:

CC ATTORNEY/AGENT INFORMATION:
CC NAME: Howells, Stacy L.
CC REGISTRATION NUMBER: 34,842
CC REFERENCE/DOCKET NUMBER: PD-2630
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 120 amino acids
CC TYPE: amino acid

CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: BOR
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..120
SQ SEQUENCE 120 AA: 12984 MW: 80846 CN:

Query Match 64 %; Score 609; DB 11; Length 120;
Best Local Similarity 72.0%; Pred. No. 1.48e-40;
Matches 90; Conservative 19; Mismatches 11; Indels 5; Gaps 2;
Db 1 VLVQSGAEVKPGSSVKYSCKASGTFSSYAISWVP-APQASIFEMSGSIPIPIFQANYA 60
QY 2 VOLLESGSEVKPGSSVKYSCKASGTFSSYFNFNWVPQAPQQLKWMQSIIPMFQIANYA 61
Db 61 QKFGQVTTITADESTNTATMELRLSRLSDTAMYYCAKESYGDY-CP-P-FLD-F--WQGGT 114
QY 62 QKFGQVTTITADESTNTATMELRLSRLSDTAMYYCAKESYGDY-CP-P-FLD-F--WQGGT 114
Db 116 VTVSS 120
QY 122 VTVSS 126

RESULT 3
ID PCT-US95-01219-45 STANDARD: PRT: 129 AA.

XX XXXXXX
AC XXXXXX
DT 01-JAN-1900

DE Sequence 45, Application PC/TUS95/01219
XX Sequence 45, Application PC/TUS95/01219
CC GENERAL INFORMATION:
CC APPLICANT: Bendig, Mary M.
CC APPLICANT: Leger, Olivier J.
CC APPLICANT: Saldanha, Jose
CC APPLICANT: Jones, S. Tarran
CC TITLE OF INVENTION: Humanized Antibodies Against leukocyte
CC TITLE OF INVENTION: Adhesion Molecule VLA-4
CC NUMBER OF SEQUENCES: 45
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kheriaty and Crew
CC STREET: One Market Plaza, Steuart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/01219
CC FILING DATE: 25-JAN-1995
CC CLASSIFICATION:

CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/216 269
CC FILING DATE: 25-JAN-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William L.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 15270-14
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9600
CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 45:
CC SEQUENCE CHARACTERISTICS:

QY 61 AOKFOGRVITTADESTATGYMELSSLRSEDYAVYYCA 97

RESULT 6
ID US-08-053-131-63 STANDARD; PRT; 102 AA.

XX xxxxxx

DT 01-JAN-1900

DE Sequence 63, Application US/08053131.

XX Sequence 63, Application US/08053131

CC Patent No. 5661016

CC GENERAL INFORMATION:

CC APPLICANT: Lonberg, Nils

CC APPLICANT: Kay, Robert M.

CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for

CC TITLE OF INVENTION: Producing Heterologous Antibodies

CC NUMBER OF SEQUENCES: 197

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Townsend and Townsend Kourie and Crew

CC STREET: One Market Plaza, Steuart Tower, Suite 200

CC CITY: San Francisco

CC STATE: California

CC COUNTRY: USA

CC ZIP: 94105

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/053.131

CC FILING DATE: 26-APR-1993

CC CLASSIFICATION: 800

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/990,960

CC FILING DATE: 16-DEC-1992

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/910,279

CC FILING DATE: 17-DEC-1991

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/853,408

CC FILING DATE: 18-MAR-1992

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Smith, William M.

CC REGISTRATION NUMBER: 30,223

CC REFERENCE/DOCKET NUMBER: 14643-9-3

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 415-326-2400

CC TELEFAX: 415-326-2422

CC INFORMATION FOR SEQ ID NO: 63:

CC LENGTH: 102 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 102 AA; 10940 MW; 55781 CN;

Query Match 62.7%; Score 595; DB 7; Length 102;
Best Local Similarity 82.5%; Pred. No. 2.14e-19;
Matches 80; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Db 5 QVOLVSGAEVKKPGSSVKVSKASGGTSSVAISWVRQAPGQGLEWMGRIPIILGIANY 64

QY 1 EVQLLESGEVRKPKGSSVKVSKASGGTSSVAISWVRQAPGQGLEWMGRIPIILGIANY 60

Db 65 AOKFOGRVITTADESTATGYMELSSLRSEDYAVYYCA 101

QY 61 AOKFOGRVITTADESTATGYMELSSLRSEDYAVYYCA 97

RESULT 7

ID PCT-US92-10983-63 STANDARD; PRT; 102 AA.

XX xxxxxx

DT 01-JAN-1900

DE Sequence 63, Application PCT/US9210983.

XX GENERAL INFORMATION:

CC APPLICANT: Lonberg, Nils

CC APPLICANT: Kay, Robert M.

CC TITLE OF INVENTION: Transgenic Non-Human Animals for

CC TITLE OF INVENTION: Producing Heterologous Antibodies

CC NUMBER OF SEQUENCES: 152

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: William M. Smith

CC STREET: One Market Plaza, Steuart Tower, Suite 2000

CC CITY: San Francisco

CC STATE: California

CC COUNTRY: USA

CC ZIP: 94105

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US92/10983

CC FILING DATE: 19921217

CC CLASSIFICATION:

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Smith, William M.

CC REGISTRATION NUMBER: 30,223

CC REFERENCE/DOCKET NUMBER: 14643-9-2

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 415-326-2400

CC TELEFAX: 415-326-2422

CC INFORMATION FOR SEQ ID NO: 63:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 102 amino acids

CC TYPE: AMINO ACID

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 102 AA; 10940 MW; 55781 CN;

Query Match 62.7%; Score 595; DB 10; Length 102;
Best Local Similarity 82.5%; Pred. No. 2.14e-19;
Matches 80; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Db 5 QVOLVSGAEVKKPGSSVKVSKASGGTSSVAISWVRQAPGQGLEWMGRIPIILGIANY 64

QY 1 EVQLLESGEVRKPKGSSVKVSKASGGTSSVAISWVRQAPGQGLEWMGRIPIILGIANY 60

Db 65 AOKFOGRVITTADESTATGYMELSSLRSEDYAVYYCA 101

QY 61 AOKFOGRVITTADESTATGYMELSSLRSEDYAVYYCA 97

RESULT 8

ID US-07-834-539A-55 STANDARD; PRT; 102 AA.

XX xxxxxx

DT 01-JAN-1900

DE Sequence 55, Application US/07834539A.

XX Sequence 55, Application US/07834539A

CC Patent No. 5633425

CC GENERAL INFORMATION:

CC APPLICANT: Lonberg, Nils

CC APPLICANT: Kay, Robert M.
 CC TITLE OF INVENTION: Transgenic No. 5633425-Human Animals Capable of
 CC TITLE OF INVENTION: Producing Heterologous Antibodies
 CC NUMBER OF SEQUENCES: 77
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: William M. Smith
 CC STREET: One Market Plaza, Stewart Tower, Suite 2000
 CC CITY: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent in Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/07/834,539A
 CC FILING DATE: 19920205
 CC CLASSIFICATION: 800
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 14643-5
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-543-9600
 CC TELEFAX: 415-543-5043
 CC INFORMATION FOR SEQ ID NO: 55:
 CC LENGTH: 102 amino acids
 CC TYPE: AMINO ACID
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE 102 AA: 10940 MW: 55781 CN:
 CC
 CC Query Match 62.7%; Score 595; DB 7; Length 102;
 CC Best Local Similarity 82.5%; Pred No 2 14e-39;
 CC Matches 80; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
 CC
 Db 5 QVQLVSGAEVKKPGSSVKVSKASGCTFSSVAISWVRCAPQGLEWGRIRPILGIANY 64
 QY 1 EVQLLESGSEVKKPGSSVKVSKASGCTFSSVAISWVRCAPQGLEWGRIRPILGIANY 60
 Db 65 AQKFGQGVITADKSTATGYMELSLRSEDATVYYCA 101
 QY 61 AQKFGQGVITADESTATGYMELSLRSEDATVYYCA 97
 CC
 CC RESULT 9
 CC ID US-08-474-040-15 STANDARD: PRT: 117 AA.
 CC XX
 CC AC xxxxxx
 CC DT 01-JAN-1900
 CC DE Sequence 15, Application US/08474040.
 CC XX
 CC Sequence 15, Application US/08474040
 CC Patent No. 5693761
 CC GENERAL INFORMATION:
 CC APPLICANT: QUEEN, Cary L.
 CC APPLICANT: CO, Man Sung
 CC APPLICANT: SCHNEIDER, William P.
 CC APPLICANT: LANDOLFI, Nicholas F.
 CC APPLICANT: COELLING, Kathleen L.
 CC APPLICANT: SELICK, Harold E.
 CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULIN
 CC NUMBER OF SEQUENCES: 113
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend Khourie and Crew
 CC STREET: 379 Lytton Avenue
 CC CITY: Palo Alto

CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94301
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent in Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/474,040
 CC FILING DATE: 07-JUN-1995
 CC CLASSIFICATION: 536
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/634,278
 CC FILING DATE: 19-DEC-1990
 CC APPLICATION NUMBER: US 07/590,274
 CC FILING DATE: 28-SEP-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/310,252
 CC FILING DATE: 13-FEB-1989
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/290,975
 CC FILING DATE: 28-DEC-1988
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 11823-002600
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 325-2400
 CC TELEFAX: (415) 325-2422
 CC INFORMATION FOR SEQ ID NO: 15:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 117 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: unknown
 CC MOLECULE TYPE: protein
 CC HYPOTHETICAL: NO
 CC FEATURE:
 CC NAME/KEY: Protein
 CC LOCATION: 1..117
 CC OTHER INFORMATION: /note: "Eu heavy chain amino acid
 CC OTHER INFORMATION: sequence."
 CC SEQUENCE 117 AA: 12472 MW: 77871 CN.
 CC
 CC Query Match 62.3%; Score 591; DB 7; Length 117;
 CC Best Local Similarity 79.0%; Pred. No. 4.58e-39;
 CC Matches 79; Conservative 11; Mismatches 10; Indels 0; Gaps 0.
 CC
 Db 1 QVQLVSGAEVKKPGSSVKVSKASGCTFSSVAISWVRCAPQGLEWGRIRPILGIANY 60
 QY 1 EVQLLESGSEVKKPGSSVKVSKASGCTFSSVAISWVRCAPQGLEWGRIRPILGIANY 60
 Db 61 AQKFGQGVITADESTATGYMELSLRSEDATVYYCAGGY 100
 QY 61 AQKFGQGVITADESTATGYMELSLRSEDATVYYCAMPY 100
 CC
 CC RESULT 10
 CC ID US-08-477-728-104 STANDARD: PRT: 117 AA.
 CC XX
 CC AC xxxxxx
 CC DT 01-JAN-1900
 CC DE Sequence 104, Application US/08477728.
 CC XX
 CC Sequence 104, Application US/08477728
 CC Patent No. 5585089
 CC GENERAL INFORMATION:
 CC APPLICANT: QUEEN, Cary L.
 CC APPLICANT: SCHNEIDER, William P.
 CC APPLICANT: SELICK, Harold E.

CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, 8th Floor
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94111
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/477,728
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 104:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 117 AA; 12472 MW; 77871 CN;

Query Match 62.3%; Score 591; DB 6; Length 117;
Best Local Similarity 79.0%; Pred. No. 4,58e-39;
Matches 79; Conservative 11; Mismatches 10; Indels 0; Caps 0;

Db 1 QVQLVQSGAEYKPKGSSVKVSKASGGTFSRSALIIWVQAPGGGLEWVGIVPMFGPPNY 60
QY 1 EVQLLESGSEVKKPKGSSVKVSKASGGGFSRSYFNWVQAPGGGLEWVGIIIPMFGTANY 60

Db 61 AOKFOGRVTITADESTNTAYMELSSLRSEDTAFYFCAGGY 100
QY 61 AOKFOGRVTITADESTATGYMELSSLRSEDTAVYYCAMPY 100

RESULT 11
ID US-08-477-728-4 STANDARD: PRT: 117 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 4, Application US/08477728.
XX
CC Sequence 4, Application US/08477728
CC Patent No. 5585089
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: SCHNEIDER, William P.

CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, 8th Floor
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94111
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/477,728
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHEICAL: NO
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..117
CC OTHER INFORMATION: /note= "Variable region of the human
CC OTHER INFORMATION: E9 antibody heavy chain."
CC SEQUENCE 117 AA; 12472 MW; 77871 CN;

Query Match 62.3%; Score 591; DB 6; Length 117;
Best Local Similarity 79.0%; Pred. No. 4,58e-39;
Matches 79; Conservative 11; Mismatches 10; Indels 0; Caps 0;

Db 1 QVQLVQSGAEYKPKGSSVKVSKASGGTFSRSALIIWVQAPGGGLEWVGIVPMFGPPNY 60
QY 1 EVQLLESGSEVKKPKGSSVKVSKASGGGFSRSYFNWVQAPGGGLEWVGIIIPMFGTANY 60

Db 61 AOKFOGRVTITADESTNTAYMELSSLRSEDTAFYFCAGGY 100
QY 61 AOKFOGRVTITADESTATGYMELSSLRSEDTAVYYCAMPY 100

RESULT 12
ID US-08-477-728-15 STANDARD: PRT: 117 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX

DE Sequence 15, Application US/08477728.
XX Sequence 15, Application US/08477728.
CC Patent No. 5585089
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, 8th Floor
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94111
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/477,728
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 15:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHEICAL: NO
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..117
CC OTHER INFORMATION: /note="Eu heavy chain amino acid
CC OTHER INFORMATION: sequence."
SQ SEQUENCE 117 AA; 12472 MW; 77871 CN;

Query Match 62.3%; Score 591; DB 6; Length 117;
Best Local Similarity 79.0%; Pred No 4 58e-19;
Matches 79; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
Db 1 QVQLVSGAEVKKPGSSVKSCASGTFSRSAIIVRWAPGGGLEWGGIVPMFGPPNY 60
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Db 61 AQKFGQGVTTITADESTATGYMELSSLSRSEDIAFYFCAGGY 100
QY 61 AQKFGQGVTTITADESTATGYMELSSLSRSEDIAVYICAMPY 100

RESULT 13
ID US-08-477-728-72 STANDARD: PRT: 117 AA.
XX xxxxxx
XX 01-JAN-1900
XX Sequence 72, Application US/08477728.
XX Sequence 72, Application US/08477728.
CC Patent No. 5585089
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, 8th Floor
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94111
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/477,728
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 72:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
SQ SEQUENCE 117 AA; 12472 MW; 77871 CN;

Query Match 62.3%; Score 591; DB 6; Length 117;
Best Local Similarity 79.0%; Pred No 4 58e-19;
Matches 79; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Db 1 QVQLVSGAEVKKPGSSVKSCASGTFSRSAIIVRWAPGGGLEWGGIVPMFGPPNY 60
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QY 61 AQKFGQGVTTITADESTATGYMELSSLSRSEDIAVYICAMPY 100

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AC xxxxxx
DT 01-JAN-1900
DE
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Sequence 15, Application US/07634278.
XX
Sequence 15, Application US/07634278.
XX
Patent No. 5530101
CC
GENERAL INFORMATION:
CC
APPLICANT: QUEEN, Cary L.
CC
APPLICANT: CO, Man Sung
CC
APPLICANT: SCHNEIDER, William P.
CC
APPLICANT: LANDOLFI, Nicholas F.
CC
APPLICANT: COELINGH, Kathleen L.
CC
APPLICANT: SELICK, Harold E.
CC
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC
NUMBER OF SEQUENCES: 113
CC
CORRESPONDENCE ADDRESS:
CC
ADDRESSEE: Townsend and Townsend Kourie and Crew
CC
STREET: 379 Lytton Avenue
CC
CITY: Palo Alto
CC
STATE: California
CC
COUNTRY: US
CC
ZIP: 94301
CC
COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
CC
COMPUTER: IBM PC compatible
CC
OPERATING SYSTEM: PC-DOS/MS-DOS
CC
SOFTWARE: Patent In Release #1.0, Version #1.25
CC
CURRENT APPLICATION DATA:
CC
APPLICATION NUMBER: US/07/634,278
CC
FILING DATE: 19-DEC-1990
CC
CLASSIFICATION: 424
CC
PRIOR APPLICATION DATA:
CC
APPLICATION NUMBER: US 07/590,274
CC
FILING DATE: 28-SEP-1990
CC
PRIOR APPLICATION DATA:
CC
APPLICATION NUMBER: US 07/310,252
CC
FILING DATE: 13-FEB-1989
CC
PRIOR APPLICATION DATA:
CC
APPLICATION NUMBER: US 07/290,975
CC
FILING DATE: 28-DEC-1988
CC
ATTORNEY/AGENT INFORMATION:
CC
NAME: Smith, William M
CC
REGISTRATION/DOCKET NUMBER: 30,223
CC
REFERENCE/DOCKET NUMBER: 11823-002600
CC
TELECOMMUNICATION INFORMATION:
CC
TELEPHONE: (415) 326-2400
CC
TELEFAX: (415) 326-3422
CC
INFORMATION FOR SEQ ID NO: 15:
CC
SEQUENCE CHARACTERISTICS:
CC
LENGTH: 117 amino acids
CC
TYPE: amino acid
CC
STRANDEDNESS: single
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MOLECULE TYPE: protein
CC
HYPOTHETICAL: NO
CC
FEATURE:
CC
NAME/KEY: Protein
CC
LOCATION: 1..117
CC
OTHER INFORMATION: /note= "Eu heavy chain amino acid
CC
OTHER INFORMATION: sequence."
SQ SEQUENCE 117 AA: 12472 MW: 77871 CN:

Query Match. 62.3%; Score 591; DB 6; Length 117;
Best Local Similarity 79.0%; Pred. No. 4,58e-39;
Matches 79; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
DB : QVQLVSGAEVKKPGSSVKVSCKASGCTFSRAIIWVQAFQGLLEWMSGLVPPMP:PPNY 60
1 EVQLLESGSEVKKPGSSVKVSCKASGCTFSRYNENVRQAPQGLFWMGGLTIPMPGTANY 60
61 AOKFQGRVTTTADSTNTAYMELSSLSRSEDIAFYFCAGGY 100
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61 AOKFQGRVTTTADSTNTAYMELSSLSRSEDIAFYFCAGGY 100
117
RESULT 15
ID US-07-634-278-4 STANDARD: PRT: 117 AA.
XX
AC xxxxxx
DT 01-JAN-1900
DE
XX
Sequence 4, Application US/07634278.
XX
Sequence 4, Application US/07634278
XX
Patent No. 5530101
CC
GENERAL INFORMATION:
CC
APPLICANT: QUEEN, Cary L.
CC
APPLICANT: CO, Man Sung
CC
APPLICANT: SCHNEIDER, William P.
CC
APPLICANT: LANDOLFI, Nicholas F.
CC
APPLICANT: COELINGH, Kathleen L.
CC
APPLICANT: SELICK, Harold E.
CC
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC
NUMBER OF SEQUENCES: 113
CC
CORRESPONDENCE ADDRESS:
CC
ADDRESSEE: Townsend and Townsend Kourie and Crew
CC
STREET: 379 Lytton Avenue
CC
CITY: Palo Alto
CC
STATE: California
CC
COUNTRY: US
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ZIP: 94301
CC
COMPUTER READABLE FORM:
CC
MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patent In Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/07/634,278
CC
FILING DATE: 19-DEC-1990
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CLASSIFICATION: 424
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/590,274
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FILING DATE: 28-SEP-1990
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/310,252
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FILING DATE: 13-FEB-1989
CC
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/290,975
CC
FILING DATE: 28-DEC-1988
CC
ATTORNEY/AGENT INFORMATION:
CC
NAME: Smith, William M
CC
REGISTRATION/DOCKET NUMBER: 30,223
CC
REFERENCE/DOCKET NUMBER: 11823-002600
CC
TELECOMMUNICATION INFORMATION:
CC
TELEPHONE: (415) 326-2400
CC
TELEFAX: (415) 326-3422
CC
INFORMATION FOR SEQ ID NO: 15:
CC
SEQUENCE CHARACTERISTICS:
CC
LENGTH: 117 amino acids
CC
TYPE: amino acid
CC
STRANDEDNESS: single
CC
MOLECULE TYPE: protein
CC
HYPOTHETICAL: NO
CC
FEATURE:
CC
NAME/KEY: Protein
CC
LOCATION: 1..117
CC
OTHER INFORMATION: /note= "Variable region of the human
CC
OTHER INFORMATION: Fc antibody heavy chain."

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SQ      SEQUENCE*      117 AA: 12472 MW: 77871 CN:
Query Match      62.3%;      Score 591;      DB 6;      Length 117;
Best Local Similarity 79.0%;      Pred. No. 4 58e-39;
Matches 79;      Conservative 11;      Mismatches 10;      Indels 0;      Gaps 0;

Db      1 QVOLVSGAEVKKPGSSVVKSCAKSGGTFSRSAIIWVPAPQGGIHWGGIVVPMFGPNY 60
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Qy      1 EVOLLESSEVKKPGSSVVKSCASGGGFSRYSFNWVQAQGGLEWGGIIPNFGTANY 60

Db      61 AOKFGQRVITIADESTNTAYMELSSLRSEDATFYFCAGGY 100
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Qy      61 AOKFGQRVITIADESTNTAYMELSSLRSEDATFYFCAGGY 100

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Search completed: Tue Feb 24 07:42:57 1998
Job time : 14 secs.



 WAREHOUSE

 (TV)

Release 2 ID John F Collins, Biocomputing Research Unit,
 Copyright (c) 1993, 1994, 1995 University of Edinburgh, U K.
 Distribution rights by IntelliGenetics, Inc.

 MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Tue Feb 24 07:16:36 1998, MasPar time 10.72 seconds
 Tabular output not generated
 Title: >US-08-844-215-7
 Description: (1-126) from US08844215 pep
 Perfect Score: 949
 Sequence: 1 EVQLLESGEVEKPKGVSKV.GSCWGFDPWGQGLTVSS 126

Scoring table: PAM 150
 Gap 11
 Searched: 111726 seqs, 13289129 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-genes30
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 30.601; Variance 151.366; scale 0.202
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	773	81.5	481	5	Sequence of antibody	2.26e-54
2	678	71.4	476	6	Antibody B heavy chain	2.50e-46
3	635	66.9	120	9	SpA-reactive IgM heavy	1.07e-42
4	634	66.8	123	23	CEA-specific antibody	1.30e-42
5	629	66.3	98	12	DP10 VH region.	3.43e-42
6	621	65.4	123	23	CEA-specific antibody	1.62e-41
7	620	65.2	123	23	CEA-specific antibody	1.97e-41
8	618	65.1	123	23	CEA-specific antibody	2.00e-41
9	617	65.0	123	23	CEA-specific antibody	2.00e-41
10	603	63.5	147	12	g3KA9 anti-Varicella	4.36e-40
11	603	63.5	249	13	Humanised 5G1.1 VH +	5.30e-40
12	598	63.0	119	23	Anti-melanoma antibody	1.39e-39
13	595	62.7	98	12	HV1263 VH region	2.49e-39
14	595	62.7	117	7	Human heavy chain V H	2.49e-39
15	595	62.7	117	4	Protein encoded by th	2.49e-39
16	595	62.7	117	20	DNA fragment vH49.8	2.49e-39
17	592	62.4	249	13	Humanised 5G1.1 VH +	4.45e-39
18	591	62.3	117	2	Human antibody Eu hea	5.40e-39
19	591	62.3	118	5	Heavy chain variable	5.40e-39
20	587	61.9	122	14	HSV-neutralising anti	1.17e-39

21	586	61.7	102	5	P25325	Hv region of human rh	1.42e-38
22	585	61.6	248	14	P77416	Humanised CDR-grafted	1.72e-38
23	581	61.2	120	9	P54795	SPA-reactive IgM heavy	3.74e-38
24	580	61.1	124	9	P45610	Monoclonal antibody G	4.53e-38
25	566	59.6	248	14	P77607	Humanised CDR-grafted	6.78e-37
26	566	59.6	249	14	P77611	Humanised 5G1.1 VH +	6.78e-37
27	563	59.3	142	9	P50188	Heavy chain variable	1.21e-36
28	559	58.9	222	7	P39267	Humanised C4G1 Ig hea	2.62e-36
29	559	58.9	235	7	P39268	Humanised C4G1 Ig hea	2.62e-36
30	554	58.9	449	7	P43339	Completely humanised	2.62e-36
31	551	58.1	142	9	P50194	Heavy chain variable	1.23e-35
32	547	57.6	468	5	P28808	pre-5A8 humanised hea	2.65e-35
33	545	57.4	121	14	P77874	Humanised mouse DRG-2	3.90e-35
34	545	57.4	149	9	P55556	Humanised alpha-4 int	1.02e-34
35	544	57.3	146	22	P22341	Monoclonal antibody G	1.24e-34
36	543	57.2	98	12	P72070	Mutated human VH1 gen	2.31e-34
37	540	56.9	119	15	P81324	CV1748RHB VH region	2.67e-34
38	540	56.9	119	23	P22425	Heavy chain variable	2.67e-34
39	539	56.9	125	9	P45409	Chimeric anti HIV ant	3.24e-34
40	536	56.5	98	6	P34372	Humanised heavy chain	3.24e-34
41	535	56.4	139	11	P62679	Heavy chain variable	3.24e-34
42	535	56.4	142	9	P50186	Humanised heavy chain	3.24e-34
43	534	56.3	118	10	P60305	Heavy chain variable	3.24e-34
44	534	56.3	140	23	P21847	Heavy chain variable	3.24e-34
45	534	56.3	142	9	P50193	Heavy chain variable	3.24e-34

ALIGNMENTS

RESULT 1
 ID R24442 standard: Protein; 481 AA.
 AC R24442;
 DT 02-JAN-1992 (first entry)
 DE Sequence of antibody molecule IgG1.
 KW Antibody; immunoglobulin G1.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc-difference 308
 FT /label= N
 FT /note= "Substn. to create glycan addition site"
 FT Misc-difference 310
 FT /label= S
 FT /note= "see above"
 FT Misc-difference 321
 FT /label= N
 FT /note= "see above"
 FT Misc-difference 329
 FT /label= N
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 FT Misc-difference 331
 FT /label= S
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 FT Misc-difference 356
 FT /label= N
 FT /note= "see above"
 FT Misc-difference 369
 FT /label= N
 FT /note= "see above"
 FT Misc-difference 379
 FT /label= N
 FT /note= "see above"
 FT Misc-difference 393-A
 FT W09292939-A
 FT 21-JUN-1992;
 FT 18-NOV-1991; US8605;
 FT 23-NOV-1990; US-518314;
 FT (GENO) GEN HOSPITAL CORP.
 FT Seed B, Walz G;
 FT WPI: 92-216789/26.
 FT N:PSDB: Q25443.
 FT Inhibition of cell adhesion mediated through ELAM-1 mol. binding
 FT - used in treating chronic inflammation, rheumatoid arthritis,
 FT psoriasis, etc.
 FT PS Disclosure; Fig 1; 46pp; English.
 FT The IgG1, in its nascent form, bears no sialyl-Lex side chains. The
 CC inventors designed a molecule including several such sites for
 CC attachment of sialyl-Lex side chains (see P24442, FI). The

(continued)

|||||
QY 121 LVTSS 126

RESULT 4
ID W19887 standard; Protein: 123 AA.
AC W19887;
DE CEA-specific antibody CEA6 VH mutant HBA11 sequence.
KW Carcinoembryonic antigen; CEA; human; antibody; scFv;
KW tumour marker; lung cancer; breast cancer; colon cancer;
KW adenocarcinoma; diagnosis.
OS Chimeric Homo sapiens;
OS Chimeric synthetic.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 50..66
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 99..112
FT /label= CDR3
FT /note= "complementarity determining region 3"
FT /note= "complementarity determining region 3"
PN W09720932-A1.
PD 12-JUN-1997.
PF 09-DEC-1996; G03043.
PP 11-OCT-1996; GB-021295.
PP 07-DEC-1995; GB-025004.
PP 23-MAY-1996; GB-010824.
PR (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Allen DJ, McCafferty JG, Osbourn JK;
DR WPI: 97-319779/29
PT Specific binding members for human carcinoembryonic antigen - bind
PT to the A3-B3 extracellular domain of hCEA and are substantially
PT non-cross-reactive with human liver cells; used for diagnosing
PT cancer
PS Claim 4; Fig 2; 128pp; English.
CC This polypeptide sequence comprises the heavy chain variable region
CC (VH), HBA11, obtained by mutagenesis of the VH CDR3 of human
CC carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see
CC W19887). A claimed specific binding member (A) comprises an hCEA
CC specific antibody antigen binding domain that has a dissociation
CC constant for hCEA of less than 1 x 10⁻⁸ M, is non-cross-reactive
CC with human liver cells, and preferentially binds to the A3-B3
CC extracellular domain of hCEA and/or to cell-associated hCEA over
CC hCEA over soluble hCEA. Preferred (A) include pairings of VH and
CC VL sequences from CEA1-7 (see W19876-85), or their CDR sequences,
CC as well as CEA6 VH and VL variants (see W19886-95) obtained by
CC mutagenesis or chain shuffling. (A) is used to detect cells
CC expressing hCEA, in vivo or in vitro, especially tumour cells for
CC diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast.
SQ Sequence 123 AA;

Query Match 66.8%; Score 634; DB 23; Length 123;
Best Local Similarity 73.0%; Pred. No. 1,306-42;
Matches 92; Conservative 19; Mismatches 12; Indels 3; Gaps 3;

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Db 61 aqkfgqrltitadeststaymelslrsdtaavyyca-g-anconrsyyy-ymdvrggct 117
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QY 61 AQKFGQRLTITADESTATGYMELSLRSDETTAVYYCAMYPKPKCSFGSCWGWEDPWGGGI 120
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Db 118 mvtvss 123
QY 121 LVTSS 126

RESULT 5
ID R72068 standard; Protein: 98 AA.

R72068;
DE 26-SEP-1995 (first entry)
DE DP10 VH region.
KW Graves ophthalmopathy associated immunoglobulin protein;
KW orbital antigen; monoclonal antibody; heavy chain; H chain;
KW variable region; autoimmunity.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT Region 50..66
FT /label= CDR2
PN W09508336-A.
PD 30-MAR-1995.
PF 22-SEP-1994; U10756.
PF 22-SEP-1993; US-124469.
DR (NICH-) NICHOLS INST DIAGNOSTICS.
PI McLachlan SM, Rapoport B;
DR WPI: 95-139383/18.
DR N-PSDB; Q89327.
PT Graves' ophthalmopathy-associated monoclonal antibody - produced
PT by molecular cloning of immunoglobulin genes by PCR
PS Disclosure; Page 68; 94pp; English.
CC L- and H-chain DNA was amplified by PCR from Graves' orbital
CC tissue and clones encoding autoimmune-associated immunoglobulin
CC fragments were obtained. 13/15 clones of H chain (IgG1) genes
CC showed homology to the closest germline genes, Dp10 (Q89327) and
CC hL263 (289328). The DNA (289329) and corresp. amino acid
CC (R72070) sequences of the VH region of a representative clone.
CC QF7H1.2, are provided.
SQ Sequence 98 AA;

Query Match 66.3%; Score 629; DB 12; Length 98;
Best Local Similarity 86.6%; Pred. No. 3,436-42;

Matches 84; Conservative 11; Mismatches 2; Indels 0; Gaps 0;
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QY 1 EVQLLESGSEVVKPGSSVKVSFASGTSFSPSYNFNVPVQAPGSGLEWMGSIIPMPFTANY 60
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Db 61 aqkfgqrltitadeststaymelslrsdtaavyyca 97
|||||
QY 61 AQKFGQRLTITADESTATGYMELSLRSDETTAVYYCA 97
|||||

RESULT 6
ID W19888 standard; Protein: 123 AA.

AC W19888;
DE 07-DEC-1997 (first entry)
DE CEA-specific antibody CEA6 VH mutant HBB11 sequence.
KW Carcinoembryonic antigen; CEA; human; antibody; scFv;
KW tumour marker; lung cancer; breast cancer; colon cancer;
KW adenocarcinoma; diagnosis.
OS Chimeric Homo sapiens;
OS Chimeric synthetic.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 50..66
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 99..112
FT /label= CDR3
FT /note= "complementarity determining region 3"
PN W09720932-A1.
PD 12-JUN-1997.
PF 09-DEC-1996; G03043.
PP 11-OCT-1996; GB-021295.
PP 07-DEC-1995; GB-025004.
PP 23-MAY-1996; GB-010824.
PR (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Allen DJ, McCafferty JG, Osbourn JK;

DR WPI: 97-319779/29.
 PT Specific binding members for human carcinoembryonic antigen - bind
 PT to the A3-B3 extracellular domain of hCEA and are substantially
 PT non-cross-reactive with human liver cells; used for diagnosing
 PT cancer
 CC Claim 4: Fig 2: 128pp: English.
 CC This polypeptide sequence comprises the heavy chain variable region
 CC (VH), HBB11, obtained by mutagenesis of the VH CDR3 of human
 CC carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see
 CC W19881). A claimed specific binding member (A) comprises an hCEA
 CC specific antibody antigen binding domain that has a dissociation
 CC constant for hCEA of less than 1 x 10⁻⁸ M, is non-cross-reactive
 CC with human liver cells and preferentially binds to the A3-B3
 CC extracellular domain of hCEA and/or to cell-associated hCEA over
 CC hCEA over soluble hCEA. Preferred (A) include pairings of VH and
 CC VL sequences from CEA1-7 (see W19876-85), or their CDR sequences,
 CC as well as CEA6 VH and VL variants (see W19886-95) obtained by
 CC mutagenesis or chain shuffling. An example of a claimed pairing
 CC is HBB11 VH with CEA6 VL. (A) is used to detect cells expressing
 CC hCEA, in vivo or in vitro, especially tumour cells for diagnosing
 CC cancer, e.g. adenocarcinoma of the colon, lung or breast.
 SQ Sequence 123 AA;

Query Match 65.4%; Score 621; DB 23; Length 123;
 Best Local Similarity 73.0%; Pred. No. 1.62e-41;
 Matches 92; Conservative 16; Mismatches 15; Indels 3; Gaps 3;

Db 1 qvqlvsgaevkpkssvkscasggtfnsplnrlrqpqgqlwmgsllpsftgany 60
 QY 1 EVQLLESGSEVKKPGSSVKVSCPSGSGSPFRSYNFWVRQAPGQGLIIPMFSTANY 60
 Db 61 aqkfggrltitadeststymelsslrdsedtavyyca-h-nh-nyelyyyyymdvwqggt 117
 QY 61 AQKFGGRVTITADESTATGYMELSLRSEDIAVYYCAMYPKHCSCGWCWFDWQGGT 120

Db 118 mvtvss 123
 QY 121 LVTVSS 126

RESULT 7

ID W19886 standard; Protein; 123 AA.
 AC W19886;
 DT 07-DEC-1997 (first entry)
 DE CEA-specific antibody CEA6 VH mutant TO6D10 sequence.
 KW Carcinoembryonic antigen; CEA; human; antibody; scFv;
 KW tumour marker; lung cancer; breast cancer; colon cancer;
 KW adenocarcinoma; diagnosis.
 OS Chimeric Homo sapiens;
 FH Chimeric synthetic.
 FT Key Location/Qualifiers
 FT Region 31...35
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 50...56
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 99...112
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 PN W09720932-AL.
 PD 12-JUN-1997.
 PF 09-DEC-1996; G03043.
 PR 11-OCT-1996; GB-021295.
 PR 07-DEC-1995; GB-025004.
 PR 23-MAY-1996; GB-010824.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Allen DJ, McCafferty JG, Osbourn JK;
 DR WPI: 97-319779/29.
 PT Specific binding members for human carcinoembryonic antigen - bind
 PT to the A3-B3 extracellular domain of hCEA and are substantially
 PT non-cross-reactive with human liver cells; used for diagnosing
 PT cancer

PS Claim 4: Fig 2: 128pp: English.
 CC This polypeptide sequence comprises the heavy chain variable region
 CC (VH), TO6D10, obtained by mutagenesis of the VH CDR3 of human
 CC carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see
 CC W19881). A claimed specific binding member (A) comprises an hCEA
 CC specific antibody antigen binding domain that has a dissociation
 CC constant for hCEA of less than 1 x 10⁻⁸ M, is non-cross-reactive
 CC with human liver cells, and preferentially binds to the A3-B3
 CC extracellular domain of hCEA and/or to cell-associated hCEA over
 CC hCEA over soluble hCEA. Preferred (A) include pairings of VH and
 CC VL sequences from CEA1-7 (see W19876-85), or their CDR sequences,
 CC as well as CEA6 VH and VL variants (see W19886-95) obtained by
 CC mutagenesis or chain shuffling. Examples of claimed pairings are
 CC TO6D10 VH with TO6D12 or CEA6 VL. (A) is used to detect cells
 CC expressing hCEA, in vivo or in vitro, especially tumour cells for
 CC diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast.
 SQ Sequence 123 AA;

Query Match 65.3%; Score 620; DB 23; Length 123;
 Best Local Similarity 72.2%; Pred. No. 1.97e-41;
 Matches 91; Conservative 16; Mismatches 16; Indels 4; Gaps 3;

Db 1 qvqlvsgaevkpkssvkscasggtfnsplnrlrqpqgqlwmgsllpsftgany 60
 QY 1 EVQLLESGSEVKKPGSSVKVSCPSGSGSPFRSYNFWVRQAPGQGLIIPMFSTANY 60
 Db 61 aqkfggrltitadeststymelsslrdsedtavyyca-qcsnyel-yyy-ymdvwqggt 117
 QY 61 AQKFGGRVTITADESTATGYMELSLRSEDIAVYYCAMYPKHCSCGWCWFDWQGGT 120

Db 118 mvtvss 123
 QY 121 LVTVSS 126

RESULT 8

ID W19889 standard; Protein; 123 AA.
 AC W19889;
 DT 07-DEC-1997 (first entry)
 DE CEA-specific antibody CEA6 VH mutant HBB6 sequence.
 KW Carcinoembryonic antigen; CEA; human; antibody; scFv;
 KW tumour marker; lung cancer; breast cancer; colon cancer;
 KW adenocarcinoma; diagnosis.
 OS Chimeric Homo sapiens;
 FH Chimeric synthetic.
 FT Key Location/Qualifiers
 FT Region 31...35
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 50...66
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 99...112
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 PN W09720932-AL.
 PD 12-JUN-1997.
 PF 09-DEC-1996; G03043.
 PR 11-OCT-1996; GB-021295.
 PR 07-DEC-1995; GB-025004.
 PR 23-MAY-1996; GB-010824.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Allen DJ, McCafferty JG, Osbourn JK;
 DR WPI: 97-319779/29.
 PT Specific binding members for human carcinoembryonic antigen - bind
 PT to the A3-B3 extracellular domain of hCEA and are substantially
 PT non-cross-reactive with human liver cells; used for diagnosing
 PT cancer
 FS Claim 4: Fig 2: 128pp: English.
 CC This polypeptide sequence comprises the heavy chain variable region
 CC (VH), HBB6, obtained by mutagenesis of the VH CDR3 of human
 CC carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see
 CC W19881). A claimed specific binding member (A) comprises an hCEA


```

DR  WFI: 95-139183/18.
DR  N-PSDB: 089328.
PT  Graves' ophthalmopathy-associated monoclonal antibody - produced
PT  by molecular cloning of immunoglobulin genes by PCR
PS  Disclosure: Page 69; 94pp; English.
CC  L- and H-chain DNA was amplified by PCR from Graves' orbital
CC  tissue and clones encoding autoimmune-associated immunoglobulin
CC  fragments were obtained. 13/15 clones of H chain (IgG1) genes
CC  showed homology to the closest germline genes, DP10 (289327) and
CC  hV1263 (289328). The DNA (289329) and corresp. amino acid
CC  (R12070) sequences of the VH region of a representative clone,
CC  OF7H1.2, are provided.
SQ  Sequence 98 AA;

Query Match 62.7%; Score 595; DB 12; Length 98;
Best Local Similarity 82.5%; Pred. No. 2 49e-39;
Matches 80; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Db 1 qvqlvsgaevkpgssvkvsckasgtfssyaisvwrqapqgglewmgriipilgiany 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1 EVOLLESGSEVKKPGSSVKVSCFASGGSFSSYFNFWFCAFGGLEWNGSIIPMFSTANY 60

Db 61 aqkfgrrvtadktsstymelsslrdsedtavyyca 97
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 AQKFGRRVTITADESTATGYMELSSLRSED TAVYYCA 97

RESULT 14
ID  R38623 standard; Protein: 117 AA.
AC  R38623;
DE  10-NOV-1993 (first entry)
DE  Human heavy chain V region VH49.8.
KW  Immunoglobulin; IgG; heavy chain; minilocus transgene;
KW  isotype switching; H chain variable region.
OS  Homo sapiens.
PN  W09312227-A.
PD  24-JUN-1993.
PF  17-DEC-1992; U10983.
PR  17-DEC-1991; US-810279.
PR  18-MAR-1992; US-853408.
PR  23-JUN-1992; US-904068.
PA  (GENP-) GENPHARM INT INC.
PI  Kay RM, Lonberg N.
PI  WPI; 93-214169/26.
DR  N-PSDB: Q44185.
PT  Transgenic non-human animals contg. immunoglobulin heavy chain
PT  trans gene - used to produce useful antibodies by isotype
PT  switching
PS  Example 12; Page 96; 196pp; English.
CC  A human placental genomic DNA library cloned into the phage vector
CC  lambda FIX II was screened with the human VH1 family specific
CC  oligonucleotide Q44184. Phage clone lambda 49.8 was isolated and a
CC  6.1kb XbaI fragment containing the variable segment VH49.8 was
CC  subcloned into pNN03 to generate plasmid pVH49.8. An 800bp
CC  region of this insert was sequenced (Q44185) and VH49.8 found to
CC  have an open reading frame and intact splicing and recombination
CC  signals, indicating that the gene is functional. Amino acid
CC  sequence Q44185 was deduced from the coding sequence; the last 3
CC  codons before the termination codon have not been translated.
SQ  Sequence 117 AA;

Query Match 62.7%; Score 595; DB 7; Length 117;
Best Local Similarity 82.5%; Pred. No. 2 49e-39;
Matches 80; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Db 20 qvqlvsgaevkpgssvkvsckasgtfssyaisvwrqapqgglewmgriipilgiany 79
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1 EVOLLESGSEVKKPGSSVKVSCFASGGSFSSYFNFWFCAFGGLEWNGSIIPMFSTANY 60

Db 80 aqkfgrrvtadktsstymelsslrdsedtavyyca 116
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 AQKFGRRVTITADESTATGYMELSSLRSED TAVYYCA 97

Search completed. Tue Feb 24 07:16:50 1998
Job time : 14 secs.

```

```

RESULT 15
ID  R22358 standard; Protein: 117 AA.
AC  R22358;
DE  17-AUG-1992 (first entry)
DE  Protein encoded by the human heavy chain V region gene VH49.8.
KW  Heavy chain; variable region; VH1 family.
OS  Homo sapiens.
PN  W09203918-A.
PD  19-MAR-1992.
PF  28-AUG-1991; U06185.
PR  29-AUG-1990; US-574748.
PR  31-AUG-1990; US-575962.
PA  (GENP-) GENPHARM INT INC.
PI  Lonberg N, Kay R,
PI  WFI; 92-113362/14.
DR  N-PSDB: Q22419.
PT  Immunoglobulin transgenes - for prodn. of heterologous
PT  non-rearranged and/or rearranged Ig chains
PS  Example 14; Page 87; 172pp; English.
CC  The human placental genomic DNA library cloned into the phage
CC  vector lambda FIX II was screened with the human VH1 family
CC  specific oligonucleotide (see Q22418). Phage clone lambda
CC  49.8 was isolated and a 6.1 kb XbaI fragment contg. the variable
CC  segment VH49.8 subcloned into pNN03 to generate plasmid pVH49.8.
CC  An 800 bp region of this insert was sequenced. VH49.8 was found
CC  to have an open reading frame which encoded the sequence shown..
SQ  Sequence 117 AA;

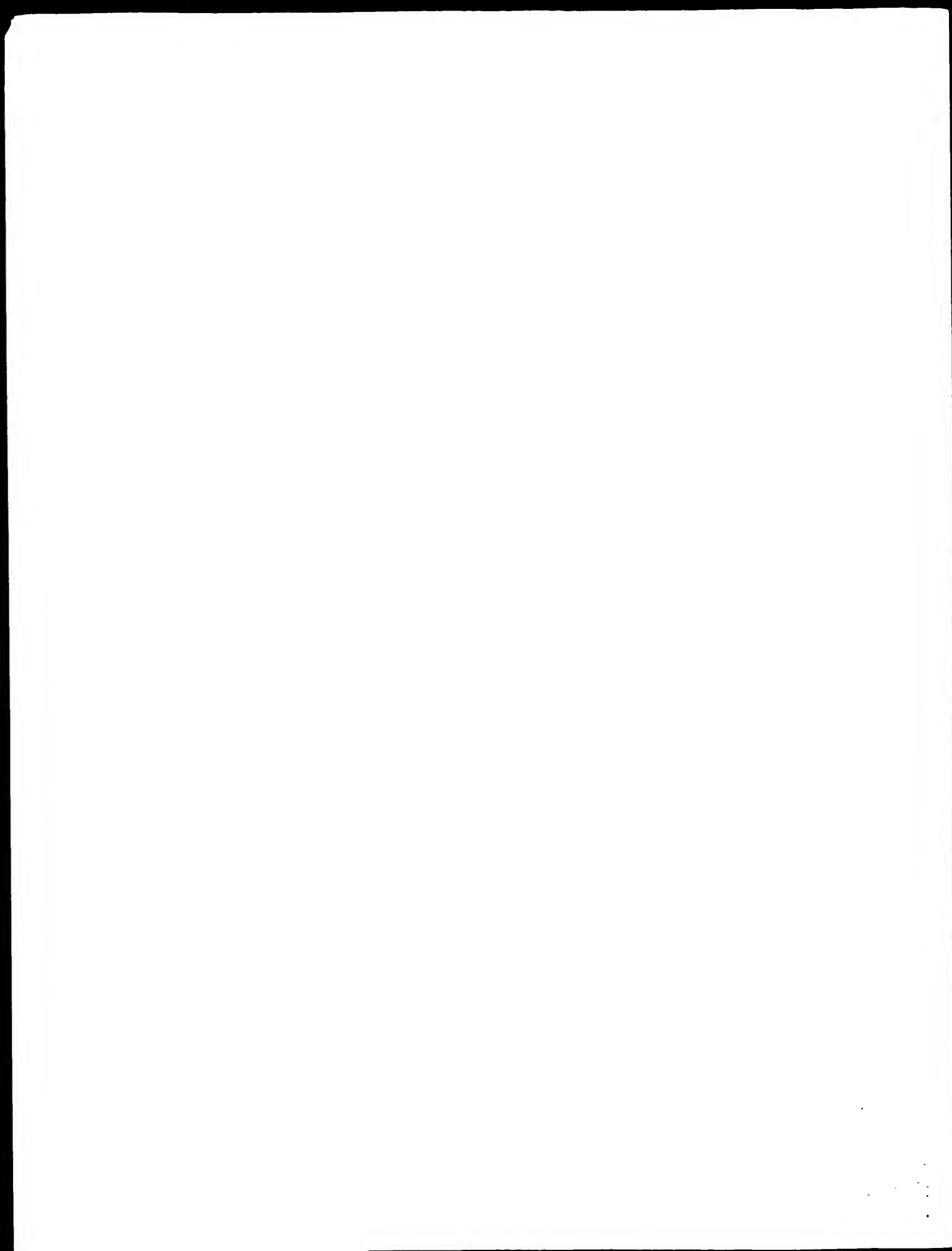
Query Match 62.7%; Score 595; DB 4; Length 117;
Best Local Similarity 82.5%; Pred. No. 2 49e-39;
Matches 80; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Db 20 qvqlvsgaevkpgssvkvsckasgtfssyaisvwrqapqgglewmgriipilgiany 79
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1 EVOLLESGSEVKKPGSSVKVSCFASGGSFSSYFNFWFCAFGGLEWNGSIIPMFSTANY 60

Db 80 aqkfgrrvtadktsstymelsslrdsedtavyyca 116
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 AQKFGRRVTITADESTATGYMELSSLRSED TAVYYCA 97

Search completed. Tue Feb 24 07:16:50 1998
Job time : 14 secs.

```



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```

MPerch_pp      protein - protein database search, using Smith-Waterman algorithm
Run on:        Tue Feb 24 07:12:56 1998;  Master time 8 23 seconds
               466.347 Million cell updates/sec
Tabular output not generated

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```
>US-08-844-215-6
Title:
Description:
(1-126) from US98044215.pdf
Perfect Score: 925
Sequence: 1 EVOLTESPGLVKPSTSL.....RMWDAFDIWGCTLVSS 126
```

Scoring table: PAM 150
Gap 11

Searched: 95051 seqs, 30469580 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

```

Database:
pir53
1-ann1 2-ann2 3-ann3 4-ann4 5-ann5 6-ann6 7-ann7
8-ann8 9-ann9 10-ann10 11-ann11 12-ann12
13-ann13 14-ann14 15-ann15 16-ann16 17-ann17
18-ann18

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description	Pred. No.	
	Score	Match	Length				
1	614	66.4	129	7	S44114	Ig heavy chain V reg	3.47e-68
2	611	66.1	130	7	S31690	Ig heavy chain V reg	9.35e-68
3	608	65.7	134	7	S34906	IgG1 heavy chain V reg	2.51e-67
4	598	64.6	98	7	S26905	Ig heavy chain V reg	6.75e-66
5	598	64.6	98	7	S12419	Ig heavy chain V reg	6.75e-66
6	597	64.5	139	7	S1586	Ig heavy chain V reg	9.39e-66
7	588	63.6	123	7	S30529	Ig heavy chain V reg	1.81e-64
8	585	63.2	140	7	I37782	Ig variable region (4.81e-64
9	583	63.0	98	7	S12417	Ig heavy chain V reg	9.39e-64
10	583	63.0	98	7	S26904	Ig heavy chain V reg	9.39e-64
11	581	62.8	130	7	S30534	Ig heavy chain V reg	1.81e-63
12	581	62.8	147	7	S13519	Ig heavy chain V reg	1.81e-63
13	575	62.2	155	7	S15522	Ig heavy chain - hum	1.36e-62
14	574	62.1	155	7	S15511	Ig heavy chain - hum	1.80e-62
15	569	61.5	146	7	S09710	Ig heavy chain V reg	9.31e-62
16	567	61.3	98	7	S12413	Ig heavy chain V reg	1.79e-61
17	567	61.3	98	7	S26903	Ig heavy chain V reg	1.79e-61
18	564	61.0	98	7	S12414	Ig heavy chain V reg	4.80e-61
19	563	60.9	135	7	S15604	Ig heavy chain V reg	6.66e-61
20	561	60.6	105	7	S44125	Ig lambda chain V re	1.29e-60

```

DATE      22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
16-Aug-1996
ACCESSIONS S31690
REFERENCE S31585
#authors Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.;
Tonnelle, C.
#submission submitted to the EMBL Data Library, June 1992
#description Mechanisms that generate human immunoglobulin diversity
operate from the 8th week of gestation in fetal liver.
#accession S31690
##status preliminary
##molecule_type mRNA
##residues 1-130 ##label CUI
##cross-references EMBL:Z14199
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
20-102
SUMMARY #domain immunoglobulin homology #label IMM
#length 130 #checksum 491

Query Match 66.1%; Score 611; DB 7; Length 130;
Best Local Similarity 73.2%; Pred. No. 9.32e-68;
Matches 93; Conservative 12; Mismatches 19; Indels 3; Gaps 3,

Db 6 qvqlqsgpglvkpsgtlsitctvsggsi-ssyvwswsrqppkqglewlgviyysgstny 64
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGPLVKPSGTLSTLCIVSGSIRSSHHWSWVRPPKGLEWGEVFFSGSTIY 60

Db 65 npslksrvtsvdknskqfslkssvtaadtavvycaargsvllwfgel-lyyfdwgg 123
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NPSLNDRVFMSVDKSDQVSLRSSVTAADTAVVYCAR-SPIKMNQGRMLDAFDIWGG 119

Db 124 lvtvss 130
||| |||
QY 120 LTVVSS 126

RESULT 3
ENTRY S54906 #type fragment
TITLE IgG1 heavy chain V region - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
09-May-1997
ACCESSIONS S54906
REFERENCE S54905
#authors Eposito, G.; Traboni, C.
#submission submitted to the EMBL Data Library, November 1994
#description Cloning and sequencing of cDNA coding for the variable
domains of a human antibody against Hepatitis C virus
helicase.
#accession S54906
##status preliminary
##molecule_type mRNA
##residues 1-134 ##label ESP
##cross-references EMBL:X82935
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY #length 134 #checksum 1180

Query Match 65.7%; Score 608; DB 7; Length 134;
Best Local Similarity 71.4%; Pred. No. 2.51e-67;
Matches 90; Conservative 12; Mismatches 23; Indels 1; Gaps 1;

Db 1 qvqlqsgpglvkpsgtlsitctvsggsinfnwnwvrtgtpkqglewlgviyysgstny 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGPLVKPSGTLSTLCIVSGSIRSSHHWSWVRPPKGLEWGEVFFSGSTIY 60

Db 61 npslksrvtsvdknskqfslkssvtaadtavvycaarg-lcsgsgscytgyfdkwgg 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NPSLNDRVFMSVDKSDQVSLRSSVTAADTAVVYCAR-SPIKMNQGRMLDAFDIWGG 120

Db 120 lvtvss 125
||| |||
QY 121 LTVVSS 126

```

```

RESULT 4
ENTRY S26905 #type fragment
TITLE Ig heavy chain V region (DP-70) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
06-Jun-1997
ACCESSIONS S26905
REFERENCE S26985
#authors Tomlinson, I.M.; Walter, G.; Marks, J.D.; Hlewozyn, M.R.;
Winter, G.
#journal J. Mol. Biol. (1992) 227:776-798
#title The repertoire of human germline V(H) sequences reveals about
fifty groups of V(H) segments with different hypervariable
loops.
#accession S26905
##status preliminary
##molecule_type DNA
##residues 1-98 ##label TOM
##cross-references EMBL:Z12370
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98
SUMMARY #domain immunoglobulin homology #label IMM
#length 98 #checksum 5975

Query Match 64.6%; Score 598; DB 7; Length 98;
Best Local Similarity 83.7%; Pred. No. 6.75e-66;
Matches 82; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Db 1 qvqlqsgpglvkpsgtlsitctvsggsissnswsvrppkqglewlgviyysgstny 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGPLVKPSGTLSTLCIVSGSIRSSHHWSWVRPPKGLEWGEVFFSGSTIY 60

Db 61 npslksrvtsvdknskqfslkssvtaadtavvycaarg 98
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NPSLNDRVFMSVDKSDQVSLRSSVTAADTAVVYCAR 98

RESULT 5
ENTRY S12419 #type complete
TITLE Ig heavy chain V region (4.19) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
06-Jun-1997
ACCESSIONS S12419
REFERENCE S09421
#authors Sanz, I.; Kelly, P.; Williams, C.; Schoell, S.; Tucker, P.;
Capra, J.D.
#journal EMBO J. (1989) 8:3741-3748
#title The smaller human V(H) gene families display remarkably
little polymorphism.
#cross-references MUID:90059975
#accession S12419
##status preliminary; translation not shown
##molecule_type DNA
##residues 1-98 ##label SAN
##cross-references EMBL:X56363
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98
SUMMARY #domain immunoglobulin homology #label IMM
#length 98 #molecular_weight 10538 #checksum 5475

Query Match 64.6%; Score 598; DB 7; Length 98;
Best Local Similarity 83.7%; Pred. No. 6.75e-66;
Matches 82; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Db 1 qvqlqsgpglvkpsgtlsitctvsggsissnswsvrppkqglewlgviyysgstny 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGPLVKPSGTLSTLCIVSGSIRSSHHWSWVRPPKGLEWGEVFFSGSTIY 60

```



```

RESULT      11
ENTRY
TITLE      Ig heavy chain V region - human
ORGANISM   Homo sapiens
DATE       06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
          16-Aug-1996
ACCESSIONS S30534 #type complete
REFERENCE   S30520
            #authors Mariette, X
            #submission submitted to the EMBL Data Library, October 1992
            #accession S30534
            ##status preliminary
            ##molecule_type mRNA
            ##residues 1-130 ##label MAR
            ##cross-references EMBL:Z18320
CLASSIFICATION
KEYWORDS   #superfamily immunoglobulin V region; immunoglobulin homology
            heterotetramer; immunoglobulin
FEATURES
            #domain immunoglobulin homology #label IMM
            #length 130 #molecular_weight 14102 #checksum 534
SUMMARY

```

	Query Match	62.8%	Score 581;	DB 7;	Length 147:
	Best Local Similarity	71.7%;	Pred. NO. 1;81c-63;		
	Matches	91;	Conservative	13;	Mismatches 16;
				Indels	7;
				Gaps	
D b	27	qlqlqesgplvkpseltlsctvtsgagssissyywqwirppkqltewlqslvyysastly #6			
Cy	1	EVCGLIESPGILVKPES-TLSLT-TVSGSISFSS-HWMSVWPQPP-KGIFWGVEFFSGSTI 59			
D b	87	yypsiksrvtisvtsdknqtisklssytaadtavvyccar-pl-lwfqe-- --fdywqqq 140			
Cy	60	YNPSLNFVFVNSVKSLGVSLTSLSVTAALTVYYCYAFSPFKNNYSEMMLLDAFDINQGQ 119			
D b	141	tltvtvss 147			
w	129	TIVTVISS 126			

```

RESULT      13
ENTRY
  TITLE      #type complete
  ID         Ig heavy chain - human
  ORGANISM   #formal_name Homo sapiens #common_name man
  DATE       13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
              16-Aug-1996
ACCESSIONS
REFERENCE
  #authors   Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
  #submission Submitted to the EMBL Data Library, December 1992
  #description Dominance of clonotypic patterns and variable gene usage in
              anti-DNA autoantibodies from patient with lupus.
  #accession S31512

```



```

#status preliminary
#molecule_type mRNA
#residues 1-155 ##label CHA
##cross-references EMBL:X69860
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
47-129 #domain immunoglobulin homology #label IMM
SUMMARY #length 155 #molecular_weight 17251 #checksum 9639

Query Match 62.1%; Score 574; DB 7; Length 155;
Best Local Similarity 66.7%; Pred. No. 1.80e-62;
Matches 84; Conservative 20; Mismatches 19; Indels 3; Gaps 3;

Db 33 qvqlqespglvkpselstictvsggsi-syyvswwirppokglewgiyytgsaty 91
QY 1 EVQLLESGPGLVKPSGTLSTCTVSGGSISSHHWSWVPPQPKGLEWGEVFFSGSTIY 60
Db 92 npplksrvltisvdknqfslkssvtaadtavvytcargg-gis-swydyymgmndvwgqgt 149
QY 61 NPSLNDRVFVMSVDKSDQVSLRLSSVTAADTAVVYCAPSPIKYNQGRMLDAFDIWGQGT 120
Db 150 tvtvss 155
QY 121 LVIVSS 126

RESULT 14
ENTRY S31511 #type complete
TITLE Ig heavy chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Aug-1996

ACCESSIONS S31511
REFERENCE S31509
#authors Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
#submission submitted to the EMBL Data Library, December 1992
#description Dominance of clonotypic patterns and variable gene usage of anti-DNA autoantibodies from patient with lupus.
#accession S31511
##status preliminary
##molecule_type mRNA
##residues 1-155 ##label CHA
##cross-references EMBL:X69866
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
47-129 #domain immunoglobulin homology #label IMM
SUMMARY #length 155 #molecular_weight 17251 #checksum 9639

Query Match 62.1%; Score 574; DB 7; Length 155;
Best Local Similarity 66.7%; Pred. No. 1.80e-62;
Matches 84; Conservative 20; Mismatches 19; Indels 3; Gaps 3;

Db 33 qvqlqespglvkpselstictvsggsi-syyvswwirppokglewgiyytgsaty 91
QY 1 EVQLLESGPGLVKPSGTLSTCTVSGGSISSHHWSWVPPQPKGLEWGEVFFSGSTIY 60
Db 92 npplksrvltisvdknqfslkssvtaadtavvytcargg-gis-swydyymgmndvwgqgt 149
QY 61 NPSLNDRVFVMSVDKSDQVSLRLSSVTAADTAVVYCAPSPIKYNQGRMLDAFDIWGQGT 120
Db 150 tvtvss 155
QY 121 LVIVSS 126

RESULT 15
ENTRY S09710 #type complete
TITLE Ig heavy chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
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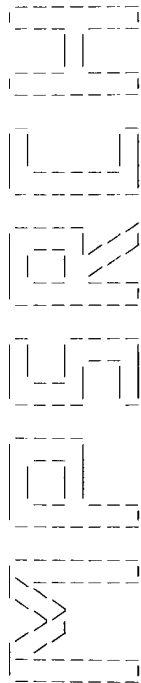
ACCESSIONS S09710
REFERENCE S09710
#authors Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
#journal Biochem. J. (1990) 268:135-140
#title Nucleotide sequences and three-dimensional modelling of the
        VH and VL domains of two human monoclonal antibodies
        specific for the D antigen of the human Rh-blood-group
        system.
#cross-references M3D:90249-35
#accession S09710
##status preliminary
##molecule_type mRNA
##residues 1-146 ##label HUG
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
34-118 #domain immunoglobulin homology #label IMM
SUMMARY #length 146 #molecular_weight 16049 #checksum 2658

Query Match 61.5%; Score 569; DB 7; Length 146;
Best Local Similarity 64.6%; Pred. No. 9.31e-62;
Matches 82; Conservative 18; Mismatches 26; Indels 1; Gaps 1;

Db 20 qirfqespglvkpselstictvsggsi-syyvswwirppokglewgiyytgsaty 79
QY 1 EVQLLESGPGLVKPSGTLSTCTVSGGSISSHHWSWVPPQPKGLEWGEVFFSGSTIY 59
Db 80 ynpslksrvltisvdknqfslkssvtaadtavvytcargg-gis-swydyymgmndvwgqgt 139
QY 50 YNPSSLNDRVFMVMSVDKSDQVSLRLSSVTAADTAVVYCAPSPIKYNQGRMLDAFDIWGQGT 119
Db 140 tvtvss 146
QY 120 LVIVSS 126

Search completed: Tue Feb 24 07:14:17 1998
Job time : 21 secs.
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100



(TM)

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mpsrch no protein - protein database search. using Smith-Waterman algorithm

Run on: Tue Feb 24 07:12:22 1998. Message time 5.58 seconds

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RUN ON:      TUE FEB 24 07:13:44 1998;
MACHINE TIME 3.33 SECONDS
478 962 Million cell updates/sec

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Title: >JCS-08-844-215-6

IIC16: 203 06 044 215 0
 Description: (1-126) from US08844215, nep

DESCRIPTION:	PERFECT SCORE:	SCORE:
1. The student can identify the main idea of a passage.	100%	92%
2. The student can identify the supporting details of a passage.	100%	95%
3. The student can identify the author's purpose in writing a passage.	100%	98%
4. The student can identify the author's tone in writing a passage.	100%	99%
5. The student can identify the author's point of view in writing a passage.	100%	100%

Sequence: 1 EVOLLESGPGLVKPSGTLSL.....RMMLDAFDIWGOGTLVIVSS 126

scoring table: PAM 150

Scoring Guide	FAM 12	Gap 11
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12

Searched: 59031 seeds. 21210398 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot34

database:
swiss_prot

8:part8 9:part9 10:part10 11:part11

Statistics: Mean 42.377; Variance 75.063; scale 0.565

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			ID	Description	Pred No.		
	Score	Match	Length					
1	549	59	4	129	5	HVCF_HUMAN	IG HEAVY CHAIN V-II S	1.90e-95
2	532	55	4	146	5	HV2L_HUMAN	IG HEAVY CHAIN PRSCUR	2.40e-87
3	471	50	9	117	5	HV2G_HUMAN	IG HEAVY CHAIN V-II P	4.07e-78
4	440	47	6	115	5	HV50_MOUSE	IG HEAVY CHAIN PRSCUR	3.39e-77
5	431	46	5	116	5	HV61_MOUSE	IG HEAVY CHAIN PRSCUR	3.41e-69
6	419	45	3	147	5	HV2H_HUMAN	IG HEAVY CHAIN PRSCUR	1.57e-66
7	417	45	1	137	5	HV46_MOUSE	IG HEAVY CHAIN PRSCUR	4.34e-66
8	408	44	1	117	5	HV62_MOUSE	IG HEAVY CHAIN PRSCUR	4.23e-64
9	407	44	0	144	5	HV43_MOUSE	IG HEAVY CHAIN PRSCUR	7.07e-62
10	398	43	0	113	5	HV47_MOUSE	IG HEAVY CHAIN V REGI	6.82e-62
11	396	42	8	116	5	HV36_MOUSE	IG HEAVY CHAIN PRSCUR	1.99e-61
12	396	42	8	119	5	HV38_MOUSE	IG HEAVY CHAIN V REGI	1.88e-61
13	396	42	8	119	5	HV37_MOUSE	IG HEAVY CHAIN V REGI	1.89e-61
14	395	42	7	119	5	HV40_MOUSE	IG HEAVY CHAIN V REGI	3.13e-61
15	386	41	7	117	5	HV41_MOUSE	IG HEAVY CHAIN V REGI	2.97e-59
16	384	41	5	116	5	HV05_CARAU	IG HEAVY CHAIN PRSCUR	6.17e-59
17	380	41	1	117	5	HV42_MOUSE	IG HEAVY CHAIN V REGI	6.15e-58
18	378	40	9	120	5	HV3E_HUMAN	IG HEAVY CHAIN V-III	1.69e-57
19	378	40	3	115	5	HV3F_HUMAN	IG HEAVY CHAIN V-III	2.10e-56
20	369	39	9	118	5	HV39_MOUSE	IG HEAVY CHAIN V REGI	1.57e-55
21	367	39	7	116	5	HV44_MOUSE	IG HEAVY CHAIN PRSCUR	4.28e-55
22	365	39	5	122	5	HV3G_HUMAN	IG HEAVY CHAIN V-III	1.17e-54

OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE; 85205332.
 RA KUDO A., ISHIMURA T., NISHIMURA Y., WATANABE T.;
 RL GENE 33:181-189(1985).
 DR PIR: A02101; GIH02.
 DR HSP: P01825; IFGV.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.

FT SIGNAL 1 19
 FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION (ARH-77).
 FT DOMAIN 20 117 V SEGMENT.
 FT DOMAIN 118 127 D SEGMENT.
 FT DOMAIN 128 146 J SEGMENT.
 FT DISULFID 42 115 BY SIMILARITY.
 FT NON_TER 146 146
 SQ SEQUENCE 146 AA; 16228 MW; 72FICBA8 CRC32.

Query Match 55.4%; Score 512; DB 5; Length 146;
 Best Local Similarity 60.6%; Pred. No. 2.40e-87;
 Matches 77; Conservative 20; Mismatches 28; Indels 2; Gaps 2.

Db 21 qvqlqwgaglvkpsqslstlctavfsgsf-sgyvswirgppqrglewqeiinhsgstny 79
 QY 1 EVQLLESGPGLVKPSTLSLTCTVSGSIRSSHHWSWVRQPPCKGLEWGEVFFSGSTII 60
 Db 80 ktslksrvtlstsknlfslkssvtaadtavvygargllrgwvndvyygmddwggg 139
 QY 61 NPSLNDRVFMSVDKSDQVSLRSSVTAADTAVVYCARSPDKMN-QGRMMLDAFDIWWGG 119
 Db 140 tvtvtvss 146
 QY 120 TLTVSS 126

RESULT 3
 ID HV2G-HUMAN STANDARD; PRT: 117 AA.
 AC P01825;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V-II REGION (NEW).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]

RP SEQUENCE.
 RX MEDLINE; 77242302.
 RA POLJAK R.J., NAKASHIMA Y., CHEN B.L., KONIGSBERG W.;
 RL BIOCHEMISTRY 16:3412-3420(1977).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
 RX MEDLINE; 78066916.
 RA SAUL F.A., AMZEL I.M., POLJAK P.J.;
 RL J. BIOL. CHEM. 253:585-597(1978).
 CC 1- THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.
 DR PIR: A02100; GIH00.
 DR PDB: 7FAB; 31-JAN-94.
 KW IMMUNOGLOBULIN V REGION; 3D-STRUCTURE.
 FT MOD_RES 1 1
 FT NON_TER 117 117
 FT STRAND 3 7
 FT STRAND 11 12
 FT TURN 14 15
 FT TURN 18 25
 FT TURN 30 31
 FT STRAND 33 39
 FT TURN 41 42
 FT STRAND 46 51
 FT TURN 53 54
 FT STRAND 57 59

FT HELIX 61 63
 FT TURN 64 66
 FT STRAND 67 72
 FT TURN 73 76
 FT STRAND 77 82
 FT HELIX 87 89
 FT STRAND 91 98
 FT STRAND 104 107
 FT STRAND 111 115
 SQ SEQUENCE 117 AA; 12790 MW; C5721B7B CRC32;
 Query Match 50.9%; Score 471; DB 5; Length 117;
 Best Local Similarity 66.3%; Pred. No. 4.03e-78;
 Matches 67; Conservative 15; Mismatches 18; Indels 1; Gaps 1.

Db 1 qvqlqsgqglvkrpsqslstlctvsgstf-sndvvtwrgppqrglewqeiinhsgstny 59
 QY 1 EVQLLESGPGLVKPSTLSLTCTVSGSIRSSHHWSWVRQPPCKGLEWGEVFFSGSTII 60
 Db 60 tplsrrvtmlvdtksqqlslrslssvtaadtavvygarnli 100
 QY 61 NPSLNDRVFMSVDKSDQVSLRSSVTAADTAVVYCARSP 101

RESULT 4
 ID HV60-MOUSE STANDARD; PRT: 116 AA.
 AC P18531;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (M315).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/CJ;
 RX MEDLINE; 89279149.
 RA LEVY N.S., MALPIERO U.V., LEHROUPE S.G., GEARHART P.J.;
 PL J. EXP. MED 169:2007-2019(1989).
 DR PIR: J0509; HYMS31.
 DR HSP: P01825; IBAF.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 18
 FT CHAIN 19 116 IG HEAVY CHAIN V REGION (M315).
 FT DOMAIN 19 48 FRAMEWORK 1.
 FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 54 67 FRAMEWORK 2.
 FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 85 116 FRAMEWORK 3.
 FT DISULFID 40 114 BY SIMILARITY.
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 13095 MW; 810F3E97 CRC32;

Query Match 47.68%; Score 440; DB 5; Length 116;
 Best Local Similarity 59.2%; Pred. No. 3.39e-71;
 Matches 58; Conservative 20; Mismatches 20; Indels 0; Gaps 0.

Db 19 dvqlqsgqglvkrpsqslstlctvsgstfsgyvwvwrqrglewqeiinhsgstny 78
 QY 1 EVQLLESGPGLVKPSTLSLTCTVSGSIRSSHHWSWVRQPPCKGLEWGEVFFSGSTII 60
 Db 79 npslksrtrtdsknqfllklnsvttedatyygar 116
 QY 61 NPSLNDRVFMSVDKSDQVSLRSSVTAADTAVVYCAR 98

RESULT 5
 ID HV61-MOUSE STANDARD; PRT: 116 AA.
 AC P18532;
 DT 01-NOV-1990 (REL. 15, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)

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DE IG HEAVY CHAIN PRECURSOR V REGION (1B43)
OS MUS MUSCULUS (MOUSE)
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: RODENTIA.
RN [1]
PP SEQUENCE FROM N A
RC STRAIN-BALB/CJ.
RX MEDLINE: 89279149.
RA LEVY N S, MALIPIERO U V, IERECQUE S G, GRAHART P J.;
RL J. EXP. MED. 169:2007-2019(1989).
CC -I- THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
DR PIR: JT0508: HVM51B.
DR HSSP: P01825: 1BAF.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION (1B43)
FT DOMAIN 19 48 FRAMEWORK 1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 54 67 FRAMEWORK 2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 85 116 FRAMEWORK 3.
FT DISULFID 40 114 BY SIMILARITY
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 13158 MW; 10E4EB67 CRC32;

Query Match 46.6%; Score 431; DB 5; Length 116;
Best Local Similarity 60.2%; Pred. No. 3,41e-69;
Matches 59; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

Db 19 dvalgespdlvkpsqlsttvtgysitsgyswhirfpgnklemgmythysgntsy 78
QY 1 EVOLLESGPLVKPSGTLSTLCTVSGSSIPSSHHWSWVPQPPKTKHLEWIGEVFFSGSTIY 60
DB 79 npslksrisitdsknqfflqlnsvttedatyycar 116
QY 61 NPSLDRVPMVDKSKDQSLSSVTAADTAIVYCAR 98

RESULT 6
ID HV2H HUMAN STANDARD: PRT: 147 AA.
AC P04438.
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 11-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-II REGION (SPSS).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE: 84298107.
RA TAKAHASHI N, NOMA T, HONJO T;
RL PROC. NATL. ACAD. SCI. U.S.A. 81:5194-5198(1984)
DR PIR: A02090: G2HUCS.
DR HSSP: P01772: LGGB.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-II REGION (SPSS)
FT DOMAIN 20 118 V SEGMENT.
FT DOMAIN 119 132 D SEGMENT.
FT DOMAIN 133 147 J SEGMENT.
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16323 MW; 0994FF54 CRC32;

Query Match 45.3%; Score 419; DB 5; Length 147;
Best Local Similarity 49.2%; Pred. No. 1,57e-66;
Matches 60; Conservative 26; Mismatches 34; Indels 2; Gaps 2;

Db 20 qvnresgpalkvathltitctfslsvntgrmsvswirppgkalewlaridwddkky 79
QY 1 EVOLLESGPLVKPSGTLSTLCTVSGSSIPSSHHWSWVPQPPKTKHLEWIGEVFFSGSTIY 59
DB 80 yatsletrltisdknqvkvltmtdpadtatyyccarmqmtmrcvymitsnrdwsgq 139

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Db 19 dvqlqesgplvksqslslctsvtgytsiysgfyfwnwlrqfpankiewlqfkydgsngy 78
Qy 1 EVOLLESGPLVKPSGTLSTCTVSGGSLRSSHWSWVRQPPKGLWIGEVFFSGSTIY 60
Db 79 npslknrvtsrtdtsknqfllksvtdtatyca 115
Qy 61 NPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYCA 97

RESULT 8
ID HV62_MOUSE STANDARD: PRT: 117 AA.
AC P18533;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (733)
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/CJ.
RX MEDLINE: 89279149.
RA LEVY N S, MALTIPIERO U V, LEBECQUE S G., GEARHART P J.,
J. EXP. MED. 169:2007-2019(1989).
DR PIR: JT0510; HVMS73.
DR HSSP: P01825; 1BAF.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 18
FT CHAIN 19 117 IG HEAVY CHAIN V REGION (733).
FT DISULFID 40 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13223 MW, 47664D8E CRC32.

Query Match 44.1%; Score 408; DB 5; Length 117;
Best Local Similarity 56.6%; Pred. No. 4.25e-64;
Matches 56; Conservative 22; Mismatches 20; Indels 1; Gaps 1.

Db 19 dvqlqesgplvksqslslctsvtgytsiysgfyfwnwlrqfpankiewlqfkydgsngy 78
Qy 1 EVOLLESGPLVKPSGTLSTCTVSGGSLRSSHWSWVRQPPKGLWIGEVFFSGSTI 59
Db 79 ynpksrtrtdtsknqfllksvtdtatyca 117
Qy 60 YNPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYCAR 98

RESULT 9
ID HV43_MOUSE STANDARD: PRT: 144 AA.
AC P01819;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (MOPC 141)
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 61012133.
RA SAKANO H., MAKI R., KUROSAWA Y., POEDER W., TONEGAWA S.;
NATURE 286:676-683(1980).
CC -!- THE SEQUENCE SHOWN IS TRANSLATED FROM A DIFFERENTIATED GENE
ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
DR EMBL: J00491; G194978;
DR EMBL: V00768; G51616;
DR PIR: A02044; G2MS14
DP HSSP: P01772; 1FDL.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 144 IG HEAVY CHAIN V REGION (MOPC 141).
FT NON_TER 144 144

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SQ SEQUENCE 144 AA; 15759 MW; 10E3A531 CRC32;

Query Match 44.0%; Score 407; DB 5; Length 144;
Best Local Similarity 53.5%; Pred. No. 7.07e-64;
Matches 66; Conservative 26; Mismatches 30; Indels 3; Gaps 3;

Db 20 qvqlkesgplvksqslslctsvtgytsiysgfyfwnwlrqfpankiewlqfkydgsngy 78
Qy 1 EVOLLESGPLVKPSGTLSTCTVSGGSLRSSHWSWVRQPPKGLWIGEVFFSGSTIY 60
Db 79 nslksrtrtdtsknqfllksvtdtatyca 137
Qy 61 NPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYCARSPKMNQGRM-MLDAFDINGOG 119
Db 138 tsvtvss 144
Qy 120 TLVIVSS 126

RESULT 10
ID HV47_MOUSE STANDARD: PRT: 113 AA.
AC P01823;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (36-60).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RC STRAIN-A/J.
RX MEDLINE: 84024551.
PA YUSZCZAK E C MAPGOLIES M N.;
BIOCHEMISTRY 22:4291-4296(1983).
CC -!- THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE MONOCLONAL ANTIBODY
OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND IDIOTYPE FAMILY
CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF STRAIN A/J MICE.
DR PIR: A02098; G2MS60.
DR HSSP: P01825; 1HEM.
KW IMMUNOGLOBULIN V REGION: ANTIARSONATE ANTIBODY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12734 MW; F18CE78F CRC32;

Query Match 43.0%; Score 398; DB 5; Length 113;
Best Local Similarity 58.8%; Pred. No. 6.83e-62;
Matches 57; Conservative 19; Mismatches 20; Indels 1; Gaps 1;

Db 1 evqlqesgplvksqslslctsvtgytsiysgfyfwnwlrqfpankiewlqfkydgsngy 59
Qy 1 EVOLLESGPLVKPSGTLSTCTVSGGSLRSSHWSWVRQPPKGLWIGEVFFSGSTIY 60
Db 60 npslksrtrtdtsknqfllksvtdtatyca 96
Qy 61 NPSLNDRVFMSVDKSKDQVSLRLSSVTAADTAVYCA 97

RESULT 11
ID HV36_MOUSE STANDARD: PRT: 116 AA.
AC P01806;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (441).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 82059449.
RA OLLO R., AUFRAY C., SIKORAV J.-I., ROUGEON F.;
NUCLEIC ACIDS RES 9:4049-4109(1981).
DR EMBL: V00774; G51651;

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Thu Feb 26 07:06:14 1998

Qy 1 EVQLLESGPGLVPSGTLSTCTVSGGSIKSSHHWSWVRQPPCKGLGLEWIGEVFFSGSTI- 59

Db 60 ytpslkdskfiisdrdnaknslylqmskvrstedtalyycar 98

Qy 60 YNPSLNDRVFMVDKSKDOVSLRLSSVTAADTAAYYCARS 98

RESULT 15
ID HV41_MOUSE STANDARD; PRT; 117 AA.
AC P01811;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1986 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (UPC10).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA AUFFRAY C., SIKORAV J.L., OLLO R., POUGEON F.;
RL ANN. INST. PASTEUR IMMUNOL. 132D:77-88(1981).
CC -!- THIS CHAIN WAS ISOLATED FROM AN IG GAMMA-2A MYELOMA PROTEIN
CC BINDING 2,6-LEVAN.
DR EMBL; M36631; G194860; -.
DR PIR; A02081; G2MSU1.
DR HSP; P01810; 1FVW.
KW IMMUNOGLOBULIN V REGION.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13001 MW; F02DB51B CRC32;

Query Match 41.7%; Score 386; DB 5; Length 117;
Best Local Similarity 54.0%; Pred. No. 2.97e-59;
Matches 54; Conservative 23; Mismatches 21; Indels 2; Gaps 2;

Db 1 evkllesgglyvpggsklscasagfd-sgywmmswvrqpgkglewigeinpdssstin 59

Qy 1 EVOLLESGPGLVPSGTLSTCTVSGGSIKSSHHWSWVRQPPCKGLGLEWIGEVFFSGSTI- 59

Db 60 ytpflkdskfiisdrdnakntlfqlmskvrstedtalyfcarn 99

Qy 60 YNPSLNDRVFMVDKSKDOVSLRLSSVTAADTAAYYCARS 99

Search completed: Tue Feb 24 07:13:38 1998
Job time : 16 secs.

WIRE

(TM)

Release 2.0 John F. Collins, Ricomputing Research Unit
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intellignetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:41:10 1998; MasPar time 3.35 Seconds

Tabular output not generated. 191.725 Million cell updates/sec

Title: >US-08-844-215-6
Description: (1-126) from US08844215.pep
Perfect Score: 925
Sequence: 1 EVQLLESGPGLVKPSTLSL RMMLDAFDINGGTLIVVSS 126

Scoring table: PAM 150

Searched: 56402 seqs, 5095871 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-issued

1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:PCT90 9:PCT91

10:PCT92 11:PCT93 12:PCT94 13:PCT95 14:PCT96

Statistics: Mean 28.331; Variance 154.255; scale 0.184

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description Pred. No.

1	559	60.4	98	7	US-08-478-	Sequence 75, Applicati	1.31e-33
2	553	59.8	126	13	PCT-US95-0	Sequence 142, Applicat	3.78e-33
3	553	59.8	126	7	US-08-276-	Sequence 142, Applicat	3.78e-33
4	533	57.6	125	7	US-08-478-	Sequence 76, Applicati	1.28e-31
5	523	56.2	121	7	US-08-478-	Sequence 80, Applicati	1.25e-30
6	509	55.0	139	7	US-08-478-	Sequence 108, Applicat	8.66e-30
7	506	54.7	121	7	US-08-275-	Sequence 13, Applicati	1.47e-29
8	502	54.3	120	6	US-08-111-	Sequence 28, Applicati	2.96e-29
9	502	54.3	120	11	PCT-US93-0	Sequence 28, Applicati	2.96e-29
10	502	54.3	120	7	US-08-211-	Sequence 28, Applicati	2.96e-29
11	500	54.1	114	11	PCT-US93-1	Sequence 16, Applicati	4.20e-29
12	478	51.7	124	7	US-08-478-	Sequence 78, Applicati	1.98e-27
13	473	51.1	119	7	US-08-478-	Sequence 77, Applicati	4.75e-27
14	471	50.9	134	6	US-08-469-	Sequence 5, Applicatio	6.74e-27
15	471	50.9	134	6	US-08-259-	Sequence 6, Applicatio	6.74e-27
16	470	50.8	116	7	US-08-478-	Sequence 79, Applicati	8.02e-27
17	464	50.2	119	13	PCT-US95-1	Sequence 62, Applicati	2.29e-26
18	462	49.9	107	7	US-07-942-	Sequence 20, Applicati	3.25e-26
19	459	49.6	119	7	US-08-467-	Sequence 62, Applicati	5.48e-26
20	459	49.6	119	7	US-08-470-	Sequence 63, Applicati	5.48e-26
21	445	48.1	129	11	PCT-US93-1	Sequence 15, Applicati	6.31e-25
22	437	47.2	114	7	US-08-211-	Sequence 23, Applicati	2.54e-24

23	437	47.2	114	11	PCT-US93-0	Sequence 23, Applicati	2.54e-24
24	437	47.2	114	6	US-08-111-	Sequence 23, Applicati	2.54e-24
25	420	45.4	147	5	US-08-468-	Sequence 8, Applicatio	4.90e-23
26	420	45.4	147	5	US-08-259-	Sequence 9, Applicatio	4.90e-23
27	419	45.3	119	7	US-08-207-	Sequence 18, Applicati	5.82e-23
28	415	44.9	120	11	PCT-US93-1	Sequence 18, Applicati	1.77e-22
29	412	44.5	125	11	PCT-US93-1	Sequence 1, Applicatio	1.96e-22
30	411	44.4	134	10	PCT-US92-0	Sequence 15, Applicati	2.34e-22
31	411	44.4	134	7	US-08-211-	Sequence 16, Applicati	2.34e-22
32	411	44.4	134	6	US-08-111-	Sequence 16, Applicati	2.34e-22
33	411	44.4	134	11	PCT-US93-0	Sequence 19, Applicati	2.34e-22
34	410	44.3	119	7	US-08-207-	Sequence 19, Applicati	2.78e-22
35	410	44.3	124	5	US-07-958-	Sequence 4, Applicatio	2.78e-22
36	410	44.3	124	11	PCT-US93-0	Sequence 4, Applicatio	2.78e-22
37	409	44.2	119	13	PCT-US95-1	Sequence 15, Applicati	3.31e-22
38	408	44.1	119	7	US-08-459-	Sequence 12, Applicati	3.91e-22
39	404	43.7	104	7	US-07-942-	Sequence 16, Applicati	7.87e-22
40	404	43.7	121	7	US-08-275-	Sequence 9, Applicatio	7.87e-22
41	404	43.7	121	11	PCT-US93-0	Sequence 20, Applicati	7.87e-22
42	404	43.7	121	7	US-08-211-	Sequence 20, Applicati	7.87e-22
43	404	43.7	121	6	US-08-111-	Sequence 20, Applicati	7.87e-22
44	404	43.7	124	11	PCT-US93-1	Sequence 44, Applicati	7.87e-22
45	403	43.6	130	7	US-08-478-	Sequence 66, Applicati	9.36e-22

ALIGNMENTS

RESULT 1 US-08-478-039-75 STANDARD: PRT: 98 AA.

XX

AC xxxxxx

DT 01-JAN-1900

DE Sequence 75, Application US/08478039.

XX Sequence 75, Application US/08478039

CC Patent No. 5681722

CC GENERAL INFORMATION

CC APPLICANT: Newman, Roland A.

CC APPLICANT: Hanna, Nabill

CC APPLICANT: Paab, Ronald W.

CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy

CC NUMBER OF SEQUENCES: 114

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

CC STREET: 699 Prince St.

CC CITY: Alexandria

CC STATE: VA

CC COUNTRY: USA

CC ZIP: 22313-1404

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent In Release #1.0, Version #1.30

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08478.039

CC FILING DATE: 07-JUN-1995

CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:

CC PRIOR APPLICATION NUMBER: US 08/379,072

CC FILING DATE: 25-JAN-1995

CC PRIOR APPLICATION DATA:

CC PRIOR APPLICATION NUMBER: US 07/312,292

CC FILING DATE: 10-JUL-1992

CC PRIOR APPLICATION DATA:

CC PRIOR APPLICATION NUMBER: US 07/856,281

CC FILING DATE: 23-MAR-1993

CC PRIOR APPLICATION DATA:

CC PRIOR APPLICATION NUMBER: US 07/735,064

CC FILING DATE: 25-JUL-1991

CC ATTORNEY/AGENT INFORMATION:

QY 4 LLESGPGLVKPSTLSLCTVSGGSRSSHWVQPPGKGLWGEVFFSGSTIYNPS 63
Db 60 LRSRTVMSPTKKNPFSVKIIVTAADTALYVCAEFTGTEIS-NEFDWGGTTLV 118
QY 64 LNDRVMSVDKSDQVSLRSSVTAADTAVVYCARSPFMNQGPMMLDAFDWGGTIV 123
Db 119 VSS 121
QY 124 VSS 126
RESULT 4
ID US-08-478-039-76 STANDARD: PRT: 125 AA.
XX XXXXX
DT 01-JAN-1900
XX
DE Sequence 76, Application US/08478039.
XX
CC Sequence 76, Application US/08478039
CC Patent No. 5681722
CC GENERAL INFORMATION:
CC APPLICANT: Newman, Roland A
CC APPLICANT: Hanna, Nabil
CC APPLICANT: Raab, Ronald W
CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
CC NUMBER OF SEQUENCES: 114
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
CC STREET: 699 Prince St.
CC CITY: Alexandria
CC STATE: VA
CC COUNTRY: USA
CC ZIP: 22313-1404
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/478,039
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/379,072
CC FILING DATE: 25-JUL-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Teskin Esq., Robin L
CC REGISTRATION NUMBER: 35,030
CC REFERENCE/DOCKET NUMBER: 012712-160
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 703-836-6620
CC TELEFAX: 703-836-2021
CC INFORMATION FOR SEQ ID NO. 76:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 125 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: not relevant
CC MOLECULE TYPE: peptide
CC ORIGINAL SOURCE:
CC ORGANISM: Monkey
CC POSITION IN GENOME:

CC CHROMOSOME/SEGMENT: VH4 clone 4-14
SQ SEQUENCE 125 AA; 13363 MW; 90929 CN;
Query Match 57.6%, Score 533, DB 7, Length 125;
Best Local Similarity 63.0%; Pred. No. 1,294-31;
Matches 80; Conservative 22; Mismatches 21; Indels 4; Gaps 4;
Db 1 QMOLESGLVKPSETLSLTCAYSGGSISSSYDWTWIRQPPGMLWIAVSGNSGSAD 60
QY 1 EVOLLESGPGLVKPSTLSLCTVSGGSRSSHWVQPPGKGLWGEVFFSGSTI 59
Db 61 YNPGLKRVITISVDTSNQPFLKMTSVTAADTALYVCAEFTGTEIS-NEFDWGGTTLV 117
QY 60 YNPGLKRVITISVDTSNQPFLKMTSVTAADTALYVCAEFTGTEIS-NEFDWGGTTLV 119
Db 118 CLVTSS 124
QY 120 TLVIVSS 126
RESULT 5
ID US-08-478-039-80 STANDARD: PRT: 121 AA.
XX XXXXX
DT 01-JAN-1900
XX
DE Sequence 80, Application US/08478039.
XX
CC Sequence 80, Application US/08478039
CC Patent No. 5681722
CC GENERAL INFORMATION:
CC APPLICANT: Newman, Roland A.
CC APPLICANT: Hanna, Nabil
CC APPLICANT: Raab, Ronald W
CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
CC NUMBER OF SEQUENCES: 114
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
CC STREET: 699 Prince St.
CC CITY: Alexandria
CC STATE: VA
CC COUNTRY: USA
CC ZIP: 22313-1404
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/478,039
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/379,072
CC FILING DATE: 25-JAN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/912,292
CC FILING DATE: 10-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/856,281
CC FILING DATE: 23-MAR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/735,064
CC FILING DATE: 25-JUL-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Teskin Esq., Robin L
CC REGISTRATION NUMBER: 35,030
CC REFERENCE/DOCKET NUMBER: 012712-160
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 703-836-6620
CC TELEFAX: 703-836-2021
CC INFORMATION FOR SEQ ID NO: 80:

US-08-844-215-6.rai

Thu Feb 26 07:06:11 1998

CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 121 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: not relevant
 CC TOPOLOGY: not relevant
 CC MOLECULE TYPE: peptide
 CC ORIGINAL SOURCE:
 CC ORGANISM: Monkey
 CC POSITION IN GENOME:
 CC CHROMOSOME/SEGMENT: VH4 anti-CD4 CHIM
 CC SEQUENCE 121 AA; 13232 MW; 88649 CN;
 SQ
 Query Match 56.2%; Score 520; DB 7; Length 121;
 Best Local Similarity 63.0%; Pred. No. 1.25e-30;
 Matches 80; Conservative 19; Mismatches 21; Indels 7; Gaps 5;
 Db 1 QVQLQAGPGLVPSQTLTSLTCSVSGSGISGDIYWFNIRQPPGKGLWIGVYSGGGTN 60
 QY 1 EVQLLESGPGLVPSQTLTSLTCTVSGGSISSSHWWSVVRQPPGKGLWIGVYSGG-TI 59
 Db 61 YNPISLNNRVISIDTSKNLFLSKLRSVTAADTAVYVCASNILKYLH-WL-L-Y--WGQG 114
 QY 60 YNPISLNDRVFMSVDKSDOVSLSSVTAADTAVYVCARSPDKMNOGRMMLDAFDINGOG 119
 Db 115 VLTVSS 121
 QY 120 TLVIVSS 126
 RESULT 6
 ID US-08-478-039-108 STANDARD; PRT; 139 AA.
 XX
 AC xxxxxx
 XX 01-JAN-1900
 DE Sequence 108, Application US/08478039.
 CC Sequence 108, Application US/08478039
 CC Patent No. 5681722
 CC GENERAL INFORMATION:
 CC APPLICANT: Newman, Roland A.
 CC APPLICANT: Raab, Ronald W.
 CC APPLICANT: Raab, Ronald W.
 CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
 CC NUMBER OF SEQUENCES: 114
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 CC STREET: 699 Prince St.
 CC CITY: Alexandria
 CC STATE: VA
 CC COUNTRY: USA
 CC ZIP: 22313-1404
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.30
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/478,039
 CC FILING DATE: 07-JUN-1995
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/379,072
 CC FILING DATE: 25-JAN-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/912,292
 CC FILING DATE: 10-JUL-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/856,281
 CC FILING DATE: 23-MAR-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/735,064

CC FILING DATE: 25-JUL-1991
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Teskin Esq., Robin L.
 CC REGISTRATION NUMBER: 35,030
 CC REFERENCE/DOCKET NUMBER: 012712-160
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 703-836-6620
 CC TELEFAX: 703-836-2021
 CC INFORMATION FOR SEQ ID NO: 108:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 139 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 139 AA; 15445 MW; 115855 CN;
 SQ
 Query Match 55.0%; Score 509; DB 7; Length 139;
 Best Local Similarity 61.9%; Pred. No. 8.66e-30;
 Matches 78; Conservative 20; Mismatches 21; Indels 7; Gaps 5;
 Db 20 QVQLQAGPGLVPSQTLTSLTCSVSGGSISSGDIYWFNIRQPPGKGLWIGVYSGGGTN 79
 QY 1 EVQLLESGPGLVPSQTLTSLTCTVSGGSISSSHWWSVVRQPPGKGLWIGVYSGG-TI 59
 Db 80 YNPISLNNRVISIDTSKNLFLSKLRSVTAADTAVYVCASNILKYLH-WL-L-Y--WGQG 133
 QY 60 YNPISLNDRVFMSVDKSDOVSLSSVTAADTAVYVCARSPDKMNOGRMMLDAFDINGOG 119
 Db 134 VLTVSS 139
 QY 120 TLVIVSS 125
 RESULT 7
 ID US-08-275-053-13 STANDARD; PRT; 121 AA.
 XX
 AC xxxxxx
 XX 01-JAN-1900
 DE Sequence 13, Application US/08275053.
 CC Sequence 13, Application US/08275053
 CC Patent No. 5607847
 CC GENERAL INFORMATION:
 CC APPLICANT:
 CC TITLE OF INVENTION: Recombinant human anti-human immunodeficiency
 CC NUMBER OF SEQUENCES: 16
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/275,053
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/GB93/01798
 CC INFORMATION FOR SEQ ID NO: 13:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 121 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 121 AA; 13365 MW; 86912 CN;
 SQ
 Query Match 54.7%; Score 506; DB 7; Length 121;
 Best Local Similarity 65.4%; Pred. No. 1.47e-29;
 Matches 83; Conservative 12; Mismatches 25; Indels 7; Gaps 4;
 Db 1 QVQLQAGPGLVPSQTLTSLTCTVSGGSISSSHWWSVVRQPPGKGLWIGVYSGGID 60
 QY 1 EVQLLESGPGLVPSQTLTSLTCTVSGGSISSSHWWSVVRQPPGKGLWIGVYSGG-TI 59

US-08-844-215-6.ra1

Thu Feb 26 07:06:11 1998

QY 60 YNPSLNDRVMSVDKSDQVSLRUSSVTAADTAVYYCARSPIKMGGRMLDAFDIWDGQ 119

Db 115 SLTVTS 120

QY 120 TLTVTS 125

RESULT 10
ID US-08-211-980-28 STANDARD: PRT: 120 AA.

XX AC xxxxxx

XX DT 01-JAN-1900

XX DE Sequence 28, Application US/08211980.

XX XX Sequence 28, Application US/08211980

CC Patent No 566556q

CC GENERAL INFORMATION:

CC APPLICANT: Ohno, Tsuneya

CC TITLE OF INVENTION: HIV Immunotherapeutics

CC NUMBER OF SEQUENCES: 38

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

CC ADDRESSEE: Borun

CC STREET: 6300 Sears Tower, 233 S. Wacker Drive

CC CITY: Chicago

CC STATE: Illinois

CC COUNTRY: USA

CC ZIP: 60606

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/211,980

CC FILING DATE:

CC CLASSIFICATION: 424

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US92/07111

CC FILING DATE: 24-AUG-1992

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/039,457

CC FILING DATE: 22-APR-1993

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Borun, Michael F.

CC REGISTRATION NUMBER: 25,447

CC REFERENCE/DOCKET NUMBER: 31629

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (312) 474-6300

CC TELEFAX: (312) 474-0448

CC TELEX: 25-3856

CC INFORMATION FOR SEQ ID NO: 28:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 120 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 120 AA: 13278 MW: 84976 CN:

Query Match 54.3% Score 502; DB 7; Length 120;
Best Local Similarity 65.1%; Pred. No. 2.96e-29;
Matches 82; Conservative 12; Mismatches 25; Indels 7; Gaps 4;

Db 1 QVQLQESGPGLVKPSQTLSTCTVSGFSTSSSYCHWVRQPPGKLEWIGRICYEGSID 60

QY 1 EVQLLESGPGLVKPSTGLSTCTVSGGSIKSSHW-WSWVRQPPGKLEWIGVFSGSTI 59

Db 61 YSPSIKSKVTMLRDTSKNPSLSSVTAADTAVYYCARE- ---NHG-TT-TSMIDYWGQ 114

QY 60 YNPSLNDRVMSVDKSDQVSLRUSSVTAADTAVYYCARSPIKMGGRMLDAFDIWDGQ 119

Db 115 SLTVTS 120

QY 120 TLTVTS 125

RESULT 11
ID PCT-US93-10555-16 STANDARD: PRT: 119 AA.

XX AC xxxxxx

XX DT 01-JAN-1900

XX DE Sequence 16, Application PC/TUS9310555.

XX XX Sequence 16, Application PC/TUS9310555

CC GENERAL INFORMATION:

CC APPLICANT: SILVERMAN, GREGG J.

CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF

CC TITLE OF INVENTION: VARIABLE REGION GENF FAMILY RESTRICTED ANTIBODIES

CC THROUGH

CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG

CC ATEs

CC TITLE OF INVENTION: THEREOF

CC NUMBER OF SEQUENCES: 51

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Spensley Horn Jubas & Lubilz

CC STREET: 1880 Century Park East Suite 500

CC CITY: Los Angeles

CC STATE: California

CC COUNTRY: USA

CC ZIP: 90067

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US93/10555

CC FILING DATE: 29-OCT-1993

CC CLASSIFICATION:

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Howells, Stacy L.

CC REGISTRATION NUMBER: 34,842

CC REFERENCE/DOCKET NUMBER: FD-2630

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (619) 455-5100

CC TELEFAX: (619) 455-5110

CC INFORMATION FOR SEQ ID NO: 16:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 119 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: peptide

CC IMMEDIATE SOURCE:

CC CLONE: LES

CC NAME/KEY: Peptide

CC LOCATION: 1..119

CC SEQUENCE 119 AA: 13135 MW: 76375 CN:

Query Match 54.1% Score 500; DB 11; Length 119;
Best Local Similarity 62.5%; Pred No 4.20e-29;
Matches 75; Conservative 16; Mismatches 27; Indels 2; Gaps 2;

Db 1 QVQLQKAGALLKFSDELSTLCVAVYGGPF-SGYVWSWYVPPKPKPWIRINISGHTTY 59

QY 1 EVQLLESGPGLVKPSTGLSTCTVSGGSIKSSHW-WSWVRQPPGKLEWIGVFSGSTI 60

Db 60 NPSLTSEVTMSLDTSKNPSLKLTSVTADTAVYYCARGPCEAYCTDAPAYFCHWGQ 119

QY 61 NPSLNDRVMSVDKSDQVSLRUSSVTAADTAVYYCARSPIKMGGRMLDA-FDIWDGQ 119

RESULT 12 US-08-478-039-78 STANDARD: PFT: 124 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 78, Application US/08478039.
XX CC Sequence 78, Application US/08478039.
XX CC Patent No. 5681722
XX CC GENERAL INFORMATION:
XX CC APPLICANT: Newman, Roland A.
XX CC APPLICANT: Hanna, Nabil
XX CC APPLICANT: Raab, Ronald W.
XX CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
XX CC NUMBER OF SEQUENCES: 114
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
XX CC STREET: 699 Prince St.
XX CC CITY: Alexandria
XX CC STATE: VA
XX CC COUNTRY: USA
XX CC ZIP: 22313-1404
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: Patent in Release #1 0, Version #1 30
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: US/08/478.039
XX CC FILING DATE: 07-JUN-1995
XX CC CLASSIFICATION: 435
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 08/379,072
XX CC FILING DATE: 25-JAN-1995
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/912,292
XX CC FILING DATE: 10-JUL-1992
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/856,281
XX CC FILING DATE: 25-JUL-1991
XX CC ATTORNEY/AGENT INFORMATION:
XX CC NAME: Teskin Esq., Robin L.
XX CC REGISTRATION NUMBER: 35,030
XX CC REFERENCE/DOCKET NUMBER: 012712-160
XX CC TELECOMMUNICATION INFORMATION:
XX CC TELEPHONE: 703-836-6620
XX CC TELEFAX: 703-836-2021
XX CC INFORMATION FOR SEQ ID NO: 78:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 124 amino acids
XX CC TYPE: amino acid
XX CC STRANDEDNESS: not relevant
XX CC TOPOLOGY: not relevant
XX CC MOLECULE TYPE: peptide
XX CC ORGANISM: Monkey
XX CC POSITION IN GENOME:
XX CC CHROMOSOME/SEGMENT: VH4 clone 4-16
XX CC SEQUENCE 124 AA: 13147 MW: 95091 CN:
Query Match 51.7%; Score 478; DB 7; Length 124;
Best Local Similarity 62.5%; Pred. No. 1.98e-27;
Matches 80; Conservative 14; Mismatches 27; Indels 7; Gaps 4;
Db 1 QVHLESGPGLVKPSTLSTCTVSGGSISSGYYWGWIPQPGKGLWIGVFEFGST 58
1 EVOLLESGPGLVKPSTLSTCTVSGGSISSGYYWGWIPQPGKGLWIGVFEFGST 58
61 SLNPSLKSRVTLSDVTSGNKFSLKSSVTAADTAATVFCAPF---LYSSSPYY--TDFWGO 115
59 IYNFSLNCPVFNVSVKDKVSIPLSSVTAADTAATVTCAPSPITKMNQGFMMILAEIDWGO 118
116 GVRVTYSS 123
119 GTLVIVSS 126
RESULT 13
ID US-08-478-039-77 STANDARD: PFT: 119 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 77, Application US/08478039.
XX CC Sequence 77, Application US/08478039
XX CC Patent No. 5681722
XX CC GENERAL INFORMATION:
XX CC APPLICANT: Newman, Roland A.
XX CC APPLICANT: Hanna, Nabil
XX CC APPLICANT: Raab, Ronald W.
XX CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
XX CC NUMBER OF SEQUENCES: 114
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
XX CC STREET: 699 Prince St.
XX CC CITY: Alexandria
XX CC STATE: VA
XX CC COUNTRY: USA
XX CC ZIP: 22313-1404
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: Patent in Release #1 0, Version #1 30
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: US/08/478.039
XX CC FILING DATE: 07-JUN-1995
XX CC CLASSIFICATION: 435
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 08/379,072
XX CC FILING DATE: 25-JAN-1995
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/912,292
XX CC FILING DATE: 10-JUL-1992
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/856,281
XX CC FILING DATE: 25-JUL-1991
XX CC ATTORNEY/AGENT INFORMATION:
XX CC NAME: Teskin Esq., Robin L.
XX CC REGISTRATION NUMBER: 35,030
XX CC REFERENCE/DOCKET NUMBER: 012712-160
XX CC TELECOMMUNICATION INFORMATION:
XX CC TELEPHONE: 703-836-6620
XX CC TELEFAX: 703-836-2021
XX CC INFORMATION FOR SEQ ID NO: 77:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 119 amino acids
XX CC TYPE: amino acid
XX CC STRANDEDNESS: not relevant
XX CC TOPOLOGY: not relevant
XX CC MOLECULE TYPE: peptide
XX CC ORIGINAL SOURCE:
XX CC ORGANISM: Monkey
XX CC POSITION IN GENOME:
XX CC CHROMOSOME/SEGMENT: VH4 clone 4-16
XX CC SEQUENCE 124 AA: 13147 MW: 95091 CN:
Query Match 51.7%; Score 478; DB 7; Length 124;
Best Local Similarity 62.5%; Pred. No. 1.98e-27;
Matches 80; Conservative 14; Mismatches 27; Indels 7; Gaps 4;
Db 1 QVHLESGPGLVKPSTLSTCTVSGGSISSGYYWGWIPQPGKGLWIGVFEFGST 60
1 EVOLLESGPGLVKPSTLSTCTVSGGSISSGYYWGWIPQPGKGLWIGVFEFGST 60

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CC CHROMOSOME/SEGMENT: VH4 clone 4-14
SQ SEQUENCE 119 AA: 12636 MW: 81453 CN:

Query Match 51.1%; Score 473; DB 7, Length 119;
Best Local Similarity 68.7%; Pred. No. 4,75e-27;
Matches 68; Conservative 11; Mismatches 19; Indels 1; Gaps 1;

Db 1 QVQLSESGPLGVKPSLTLCAVSGSSISSGGYWGNIQTTPGKGLWIGSLQPGSGNKY 60
QY 1 EVQLLESGPLGVKPSGLTSLTCTVSGSIRSSHWSWYRQPPGKGLWIGEVFFSGSTIY 60
Db 1 LNLCLKSRVTLSDTSKNQFSLKLSSTVAADTAVYYCAR 99
QY 1 NPSLNDRVFNSVDKSKDQVSLKLSSTVAADTAVYYCAR 98

RESULT 14
ID US-08-468-671-6 STANDARD: PRT: 134 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 6, Application US/08468671.
XX
EX Patent 6, Application US/08468671
CC Patent No. 5648077
CC GENERAL INFORMATION:
CC APPLICANT: Ostberg, Lars G.
CC TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
CC TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIG
EN
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, Eighth Floor
CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.30
CC SOURCE APPLICATION DATA:
CC CURRENT APPLICATION NUMBER: US/08/468,671
CC APPLICATION NUMBER: US/08/468,671
CC FILING DATE: 06-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/259,372
CC FILING DATE: 14-JUN-1994
CC APPLICATION NUMBER: US 07/871,426
CC FILING DATE: 21-APR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/676,036
CC FILING DATE: 27-MAR-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/538,796
CC FILING DATE: 15-JUN-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/192,754
CC FILING DATE: 11-MAY-1988
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/925,196
CC FILING DATE: 31-OCT-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/904,517
CC FILING DATE: 05-SEP-1986
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-50-7

```

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 134 AA: 14995 MW; 109187 CN;

Query Match      50.9%; Score 471; DB 7; Length 134;
Best Local Similarity 69.7%; Pred. No. 6.74e-27; Indels 1; Gaps 1;
Matches 69; Conservative 11; Mismatches 18;

db    20 QVQLSESGPLGVKAAETLSLCTYSRGSF-SDYFWNNWFRQAGKRLKLEMLGRVTYSGSVDY 78
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Qy    1 ECVLSESGPLGVKPSGTLISLCTYSGSIRSHHMSWVRPPGKGLEIWGEVFTSGSTIY 60

Db    79 NPSLKSRVTYSVDTSKKQFSKLSSLTVAADTAVYYCARG 117
      :|||: || |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy    61 NFSLNDRVPMVSVDKSKDOVSLRSLSSVTADTAVYYCAR 99

RESULT 15          STANDARD:           PRT:   134 AA.
ID       US-08-259-372A-6
XX       xxxxxx
AC       XX
XX       XX
DT       01-JAN-1900
XX       XX
UE       Sequence 6, Application US/08259372A.
CC       Sequence 6, Application US/08259372A
CC       Patent No. 5565354
CC       GENERAL INFORMATION:
CC       APPLICANT: Ostberg, Lars G.
CC       TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
CC       TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
CC       EN

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
FILING DATE: 14-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,036
FILING DATE: 27-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
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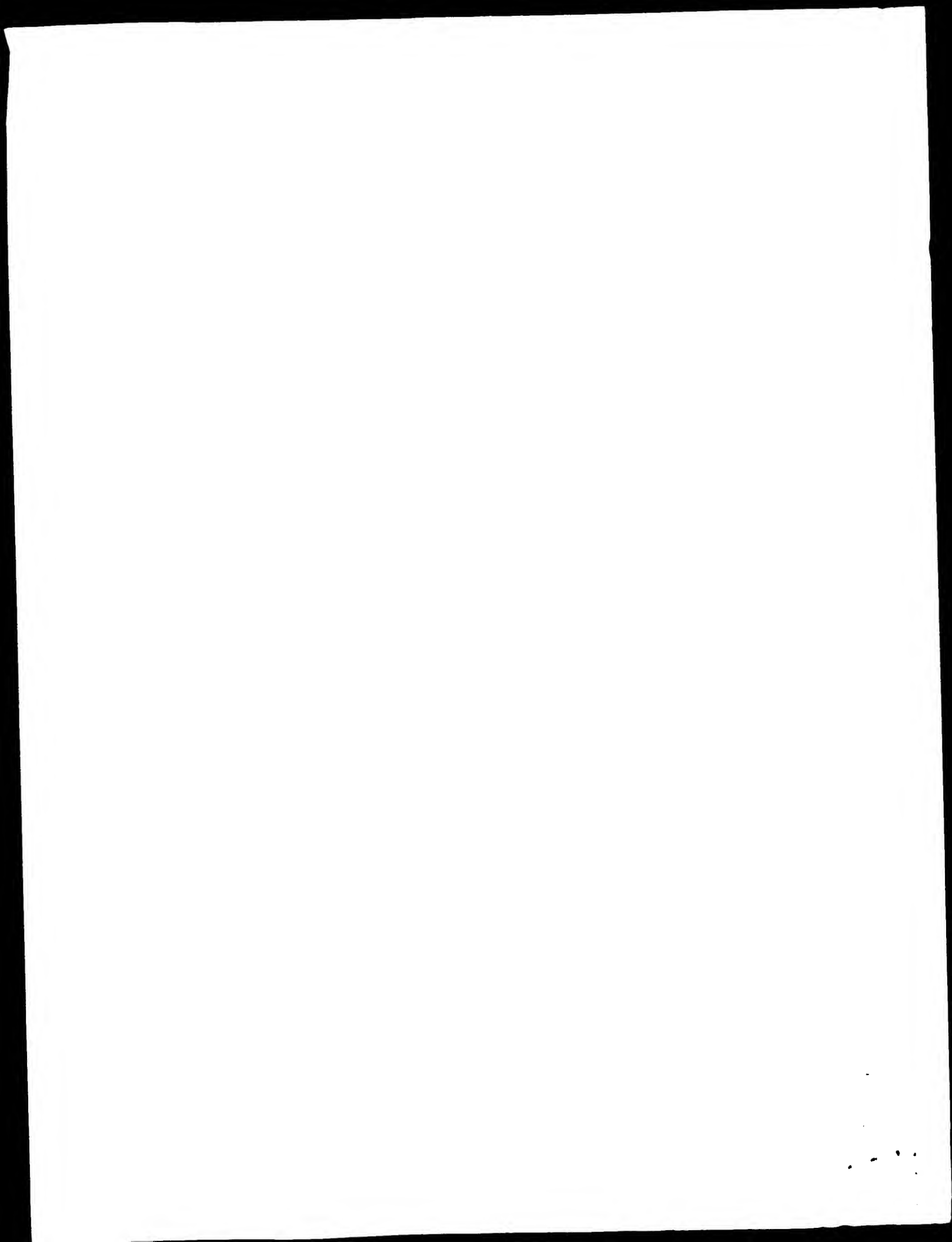
CC * APPLICATION NUMBER: US 06/904,517
CC FILING DATE: 05-SEP-1986
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-50-7
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 576-0300
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 134 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 134 AA: 14995 MW: 109187 CN;

Query Match 50.9%, Score 471, DB 6, Length 134,
Best Local Similarity 69.7%; Pred. NO. 6.74e-27;
Matches 69; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

Db 20 QVQLQESGPGLVKAAETLSLTCTVSRGSF-SDYFNNWFQPAKPLEWGPVYTSSSVTY 78
QY :||| |||||: ||||| ||: | ||: ||||| ||: ||| |
1 EYQLLESGPLVKPGTSLTCTVSGGSIRSSHWSVVRQPPKGLWIGVFFSGTIY 60
|||: || ||| || ||||| ||||| |||:
Db 79 NPSLKSRTVSVDTSKKQFSLRLSSVTIVADTAVYYCARG 117
|||: || ||| || ||||| ||||| |||:
QY 61 NPSLNDRVFMSVDKSKDQVSLRLSSVTIADTAVYYCARS 99

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Search completed: Tue Feb 24 07:41:23 1998
Job time : 13 secs.



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FT	FT	Region			1..26
FT	FT	/label= FR1			
FT	FT	/note= "framework region"			
FT	FT	Region			27..36
FT	FT	/label= CDR1			
FT	FT	Region			37..50
FT	FT	/label= FR2			
FT	FT	/note= "framework region"			
FT	FT	Region			51..56
FT	FT	/label= CDR2			
FT	FT	Region			67 98
FT	FT	/label= FR3			
FT	FT	/note= "framework region"			
FT	FT	Region			99..106
FT	FT	/label= CDR3			
FT	FT	Region			107..117
FT	FT	/label= FR4			
FT	FT	/note= "framework region"			
FT	FT	Region			118..126
FT	FT	/label= CDR4			
FT	FT	Region			127..136
FT	FT	/label= FR5			
FT	FT	/note= "framework region"			
FT	FT	Region			137..145
FT	FT	/label= CDR5			
FT	FT	Region			146..154
FT	FT	/label= FR6			
FT	FT	/note= "framework region"			
FT	FT	Region			155..163
FT	FT	/label= CDR6			
FT	FT	Region			164..172
FT	FT	/label= FR7			
FT	FT	/note= "framework region"			
FT	FT	Region			173..181
FT	FT	/label= CDR7			
FT	FT	Region			182..190
FT	FT	/label= FR8			
FT	FT	/note= "framework region"			
FT	FT	Region			191..199
FT	FT	/label= CDR8			
FT	FT	Region			200..208
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FT	FT	/note= "framework region"			
FT	FT	Region			209..217
FT	FT	/label= CDR9			
FT	FT	Region			218..226
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FT	FT	/note= "framework region"			
FT	FT	Region			227..235
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FT	FT	Region			236..244
FT	FT	/label= FR11			
FT	FT	/note= "framework region"			
FT	FT	Region			245..253
FT	FT	/label= CDR11			
FT	FT	Region			254..262
FT	FT	/label= FR12			
FT	FT	/note= "framework region"			
FT	FT	Region			263..271
FT	FT	/label= CDR12			
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FT	FT	Region			281..289
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FT	FT	/label= FR14			
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FT	FT	Region			299..307
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FT	FT	Region			308..316
FT	FT	/label= FR15			
FT	FT	/note= "framework region"			
FT	FT	Region			317..325
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FT	FT	Region			326..334
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FT	FT	Region			335..343
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FT</					

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DR WPI: 93-288411/36.
PT New altered antibodies with reduced immune responses - have
PT germ-line aminoacid residues replacing somatically mutated
PT residues
PS Example 3; Fig 4a; 53pp; English.
CC A humanised antibody comprised CDRs originally from a mouse Mab
CC PSV19 specific for Respiratory Syncytial Virus transplanted onto
CC heavy and light chain V region domains derived from NEWM and REI
CC myeloma proteins, respectively. The framework regions of this
CC CDR-grafted antibody were converted to the germ-line equivalent
CC For conversion of the H-chain, the germ-line heavy chain DP68/JH6
CC (R40953) was used. Germ-line framework regions are those present in
CC immature B cells, i.e. prior to any somatic mutation which takes
CC place during maturation. Unlike mutations in the CDRs, any mutation
CC in framework regions does not affect affinity for an antigen and is
CC therefore essentially random. The mutation may, however, cause the
CC "self" antibody to be recognised as "foreign" and conversion to the
CC unmutated germ-line sequence renders the framework regions "immuno
CC silent".
SQ Sequence 117 AA;

Query Match 61.3%; Score 567; DB 8; Length 117.
Best Local Similarity 77.6%; Pred. No. 4.15e-33;
Matches 76; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Db 1 qvqlqesgplvksdltscavsgysissnwwgwtgppdkglewlglyvysgstyy 60
QY 1 EVQLLESGPGLVPSGTLSTLTCTVSGQSIPSSHHWMSWVPQPPKGLGLEWIGVFSSGSIY 60

Db 61 npslndrvfmsvdknqfslklsstvtavdtavyycaar 98
QY 61 NPSLNDRVFMSVDKNSKQVSLPISSVTAADTAVVYCAP 99

RESULT 5
ID R12265 standard; Protein: 124 AA
AC R12265;
DE Anti-human RHD PAG-1 Mab (VH chain)
KW Monoclonal antibody; rhesus D; blood-typing; CDR;
KW haemolytic disease of the newborn; HDN.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT Region 50 65
FT /label= CDR2
FT Region 98 113
FT /label= CDR3
FT WO9107492-A.
PD 30-MAY-1991.
PF 13-NOV-1990; E01964.
PR 13-NOV-1989; GB-025590.
PA (BLOO-) CENT BLOOD LAB AUTH.
PI Hughes- Jones N;
DP WPI: 91-178104/24.
DN N-PSDR: Q11948.
PT DNA encoding complementary determining regions - of human
PT anti-rhesus D antibodies, useful in prodn. of monoclonal
PT antibodies and for passive immunisation
PS Disclosure: Fig 5; 32pp; English.
CC The DNA sequence of eleven monoclonal antibodies are
CC represented in Q119145-57. Synthetic genes, for both heavy and
CC light chains may be created by combining selected CDR 1, 2, and 3
CC regions, which may be selected from different antibody mols. having
CC varied binding specificity. The chimaeric anti-Rhd antibodies can be
CC used for diagnosis and therapy, and are capable of providing blood-
CC typing reagents of high specificity and reliability. They can also
CC be used in passive immunisation to prevent haemolytic disease of the
CC newborn.
SQ Sequence 124 AA;

Query Match 60.4%; Score 559; DB 2; Length 124;
Best Local Similarity 63.8%; Pred. No. 1.99e-32;
Matches 81; Conservative 18; Mismatches 27; Indels 1; Gaps 1;

Db 1 qlrlqesgplvksdltscavsgysgssgglvkwgwwirppqkglewlgisfygssty 60
QY 1 EVQLLESGPGLVPSGTLSTLTCTVSGQSIPSSHHWMSWVPQPPKGLGLEWIGVFSSGSIY 59

Db 61 npslndrvfmsvdknqfslklsstvtavdtavyycaar 120
QY 61 NPSLNDRVFMSVDKNSKQVSLPISSVTAADTAVVYCAP 119

Db 121 tvtvss 127
QY 120 TLIVSS 126

RESULT 7
ID P03552 standard; Protein: 475 AA.

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SQ Sequence 126 AA;

Query Match 59.8%; Score 553; DB 10; Length 126;
 Best Local Similarity 66.7%; Pred No 4 770-32;
 Matches 82; Conservative 14; Mismatches 25; Indels 2; Gaps 2;

Db 1 llesgplvxpsetlsictvsgsissfdw-nwirgpaqkalewigriypsgnthynps 59
 QY 4 LLESGPLVXPSETLSICTVSGSISRSHHWSWVQPPKGLEWIGEVFFSGSTIYNPS 63

Db 60 lrsrvmsrdtsknqfsvkltsytaadtalyccarentgtrticeig-nffdiwgqgtlvt 118
 QY 64 LNDREVMSVDKSDQVSLRSSVTAADTAVVYCAPSPIKWNQPMMLDAFTDWGQGTTLVI 123

Db 119 vss 121
 QY 124 VSS 126

RESULT 10 Location/Qualifiers
 ID W01315 standard; Protein: 126 AA
 AC W01315; 1997 (first entry)
 DT 29-JAN-1997
 DE VH of Fab DL 41 19, binds to HIV gp41.
 KW Heavy chain; light chain; variable region; VH; monoclonal antibody;
 KW MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;
 KW virus infectivity assay; precursor gp160; immunocompetence; human;
 KW anti-HIV antibody; detection: HIV infection.
 OS Homo sapiens.
 FH Key
 FT Region 1..27 Location/Qualifiers
 FT /label= FR1
 FT Region 28..32
 FT /label= CDR1
 FT Region 33..46
 FT /label= FR2
 FT Region 47..52
 FT /label= CDR2
 FT Region 63..94
 FT /label= FR3
 FT Region 95..110
 FT /label= CDR3
 FT Region 111..126
 FT /label= FR4
 PN W09602273-A1.
 PD 01-FEB-1996
 PR 11-JUL-1995; U08743.
 PR 18-JUL-1994; US-276852.
 PA (SCR1) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 DR WPI: 96-179601/18.
 PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in
 PT passive immunotherapy and detection of HIV infection.
 PS Example 3; Fig 18; 366pp; English.
 CC The sequences given in W01315-19 represent the heavy chain variable
 CC regions (VH) of a series of antibody fragments (Fab's) which are
 CC immunoreactive with HIV glycoprotein gp41. This sequence represents
 CC the sequence of the clone, DL 41 19. These sequences represent heavy
 CC chains which bind to the light chain clones given in W01320-24. A
 CC monoclonal antibody containing one of these Fab sequences may have the
 CC capacity to reduce HIV infectivity titre in an in vivo virus infectivity
 CC assay by 50 % at a concentration of less than 700 ng of antibody/ml.
 CC The MAb may be used for determining immunocompetence of a human anti-HIV
 CC antibody and in the detection of HIV infection.
 SQ Sequence 126 AA;

Query Match 59.8%; Score 553; DB 19; Length 126;
 Best Local Similarity 66.7%; Pred No 4 770-32;
 Matches 82; Conservative 14; Mismatches 25; Indels 2; Gaps 2;

Db 1 llesgplvxpsetlsictvsgsissfdw-nwirgpaqkalewigriypsgnthynps 59
 QY 4 LLESGPLVXPSETLSICTVSGSISRSHHWSWVQPPKGLEWIGEVFFSGSTIYNPS 63

Db 60 lrsrvmsrdtsknqfsvkltsytaadtalyccarentgtrticeig-nffdiwgqgtlvt 118
 QY 64 LNDREVMSVDKSDQVSLRSSVTAADTAVVYCAPSPIKWNQPMMLDAFTDWGQGTTLVI 123

Db 119 vss 121
 QY 124 VSS 126

RESULT 12 Location/Qualifiers
 ID R66346 standard; Protein: 116 AA.
 AC R66346;
 DT 04-AUG-1995 (first entry)
 DE Human immunoglobulin; variable heavy chain #52.
 KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain.
 KW cosmid; placenta; vector; pDB81; E.Coli; mammalian.
 OS Homo sapiens.
 PN W09425695-A.

Db 60 lrsrvmsrdtsknqfsvkltsytaadtalyccarentgtrticeig-nffdiwgqgtlvt 118
 QY 64 LNDREVMSVDKSDQVSLRSSVTAADTAVVYCAPSPIKWNQPMMLDAFTDWGQGTTLVI 123

Db 119 vss 121
 QY 124 VSS 126

RESULT 11 Location/Qualifiers
 ID R42689 standard; Protein: 116 AA.
 AC R42689;
 DT 01-NOV-1993 (first entry)
 DE VH 71-4.
 KW Monoclonal antibody, MAb; envelope, glycoprotein; gp120; HIV; AIDS;
 KW CD4; receptor; hyridoma; polymerase chain reaction; PCR; heavy; light;
 KW chain; epitope; immune deficiency.
 OS Homo sapiens.
 FH Key
 FT Peptide 1..19 Location/Qualifiers
 FT /label= sig_peptide
 FT Protein 20..116
 FT /label= mat_protein
 FT Region 49..54
 FT /label= CDR1
 FT Region 69..84
 FT /label= CDR2
 PN W09312232-A.
 PD 24-JUN-1993.
 PR 10-DEC-1992; U10928.
 PR 10-DEC-1991; US-804652.
 PA (DAND) DANA FAPRER CANCER INST INC.
 PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
 PI Haseltine WA, Marasco WA, Posner MP, Sodroski JG;
 DR WPI: 93-214174/26.
 DR N-FSDB: Q42697.
 FT DNA segments encoding monoclonal antibody - which binds to gp120
 FT and neutralises HIV, for treating AIDS, and for diagnosing and
 FT monitoring HIV infection
 PS Disclosure; Page 64; 109pp; English.
 CC The nucleotide sequence of rearranged F105 Vh (Q42698) was compared
 CC to two monoclonal antibodies (AB26 - Q42702) and 288-D - Q42703),
 CC which by nucleotide sequence analysis, appear to use a rearranged
 CC Vh 71-4 gene (Q42697).
 CC AB26 (Q42702) was derived from CD5+ B cells of a healthy donor and
 CC represents a naturally occurring polyreactive antibody which binds to
 CC many antigens. AB26 shares greatest sequence similarity with germline
 CC Vh 71-4.
 SQ Sequence 116 AA;

Query Match 59.5%; Score 550; DB 7; Length 116;
 Best Local Similarity 78.6%; Pred. No. 8 04e-32;
 Matches 77; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

Db 20 gvlqgesgplvxpsetlsictvsgsissfdw-nwirgpaqkalewigriypsgntny 78
 QY 1 EVQLLESGPLVXPSETLSICTVSGSISRSHHWSWVQPPKGLEWIGEVFFSGSTIY 60

Db 79 npslksrvtlsvdtskqfalklssttaadtavvyar 116
 QY 61 NPSLKSrvtlsvdtskqfalklssttaadtavvyar 98

RESULT 12 Location/Qualifiers
 ID R66346 standard; Protein: 116 AA.
 AC R66346;
 DT 04-AUG-1995 (first entry)
 DE Human immunoglobulin; variable heavy chain #52.
 KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain.
 KW cosmid; placenta; vector; pDB81; E.Coli; mammalian.
 OS Homo sapiens.
 PN W09425695-A.

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PD 24-NOV-1994
PF 10-MAY-1993; J00603.
PA (NIBS) JAPAN TOBACCO INC.
PI Honjo T., Matsuda F.
DR WPI: 95-006791/01.
PT DNA fragment comprising human immunoglobulin Vh genes - for the
PT production of human immunoglobulin in mammalian hosts
PS Disclosure: Page 107-108; 130pp; Japanese.
CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain
CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were
CC isolated and cloned from a series of cosmid constructs. Y202; Y103; Y21;
CC Y6; Y24; 3-31; M84; M18 and M131, by PCR amplification using primers
CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The
CC fragments cover a region of 800 kb. The DNA fragments were isolated from
CC high molecular weight DNA from human placenta. The DNA was partially
CC digested with TaqI restriction enzyme. The fragments were separated by
CC gel electrophoresis and 35-45 kb fractions were collected. The fragments
CC were ligated with ClaI-digested cosmid vector pJB81. The ligation
CC products were in vitro packed and infected into E.coli 490A. The
CC fragments were then subcloned by colony hybridisation. The Vh genes and
CC the DNA fragments encoding them are useful in producing human
CC immunoglobulin in mammalian hosts.
SQ Sequence 116 AA.

Query Match 59.5%; Score 550; DB 12; Length 116;
Best Local Similarity 78.6%; Pred. No. 8,04e-32;
Matches 77; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

Db 20 qvqlqesgpglvkpsktslctvsgsgvssyyvswirppqkglewlyiyysgstny 78
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 EVQLLESGPGLVKPSGTLSTCTVSGSIRSSHWSWVRQPPGKGLEWIGVEFFSGSTIY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 79 npslksrvtsvdktskqfklssvtaadtavyycar 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 NPSSLNDRVFMVSKDQVSLRSLSSVTAADTAVYYCAR 98

RESULT 13
ID W01822 standard; Protein: 476 AA.
AC W01822;
DE 25-MAY-1997 (first entry)
KW Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KW primatised antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma.
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
PN W09640878-A1.
PD 19-DEC-1996.
PF 06-JUN-1996; U10053.
PR 07-JUN-1995; US-487550.
PA (IDEC-) IDEC PHARM CORP.
PI Anderson DR, Brams P, Hanna N, Shetowsky WS.
DR WPI: 97-108638/10.
DR N-PSDB: T62513.
PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT useful for treating autoimmune disease or graft-versus-host disease
PS Claim 14; Fig 10B; 81pp; English.
CC 2 Polypeptides (W01821 and W01822) respectively comprise primatised
CC forms of the light and heavy chains of cynomolgus monkey anti-human
CC B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and
CC heavy variable genes (see also T62512 and T62513) are inserted into
CC an expression vector (pref. NCS-SPLA) which contains human light and
CC heavy chain constant region genes to allow prodn. of the primatised
CC antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1
CC antibodies have also been produced (see also W01817-20). The
CC primatised antibodies inhibit the B7:CD28 pathway, making them
CC useful immunosuppressants for the treatment of autoimmune disorders

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CC and graft-versus-host disease.
SQ Sequence 476 AA;

Query Match 59.5%; Score 550; DB 20; Length 476;
Best Local Similarity 52.5%; Pred. No. 8,04e-32;
Matches 80; Conservative 19; Mismatches 26; Indels 4; Gaps 1;

Db 20 qvqlqesgpglvkpsktslctvsgsgvssyyvswirppqkglewlyiyysgstny 79
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Qy 1 EVQLLESGPGLVKPSGTLSTCTVSGSIRSSHWSWVRQPPGKGLEWIGVEFFSGSTI 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 80 ynpslksrvtsvdktskqfklssvtaadtavyycvdrilfsvvg-mvynunwfdwvq 138
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 60 YNPSSLNDRVFMVSKDQVSLRSLSSVTAADTAVYYCARPKMKNOGRMMLDA-FDIWQ 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 139 gvlvtvss 146
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 119 GFLVIVSS 126
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
ID R66348 standard; Protein: 118 AA.
AC R66348;
DE 04-AUG-1995 (first entry)
KW Human immunoglobulin variable heavy chain #54.
DE Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
KW cosmid; placenta; vector; pJB81; E.coli; mammalian.
OS Homo sapiens.
PN W09426895-A.
PD 24-NOV-1994.
PF 10-MAY-1993; J00603.
PR 10-MAY-1993; WO-J00603.
PA (NIBS) JAPAN TOBACCO INC.
PI Honjo T., Matsuda F.
DR WPI: 95-006791/01.
DR N-PSDB: Q78999.
PT DNA fragment comprising human immunoglobulin Vh genes - for the
PT production of human immunoglobulin in mammalian hosts
PS Disclosure: Page 110-111; 130pp; Japanese.
CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain
CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were
CC isolated and cloned from a series of cosmid constructs. Y202; Y103; Y21;
CC Y6; Y24; 3-31; M84; M18 and M131, by PCR amplification using primers
CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The
CC fragments cover a region of 800 kb. The DNA fragments were isolated from
CC high molecular weight DNA from human placenta. The DNA was partially
CC digested with TaqI restriction enzyme. The fragments were separated by
CC gel electrophoresis and 35-45 kb fractions were collected. The fragments
CC were ligated with ClaI-digested cosmid vector pJB81. The ligation
CC products were in vitro packed and infected into E.coli 490A. The
CC fragments were then subcloned by colony hybridisation. The Vh genes and
CC the DNA fragments encoding them are useful in producing human
CC immunoglobulin in mammalian hosts.
SQ Sequence 118 AA;

Query Match 59.4%; Score 549; DB 12; Length 118;
Best Local Similarity 77.8%; Pred. No. 9,57e-32;
Matches 77; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

Db 20 qvqlqesgpglvkpsktslctvsgsgvssyyvswirppqkglewlyiyysgstny 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 EVQLLESGPGLVKPSGTLSTCTVSGSIRSSHWSWVRQPPGKGLEWIGVEFFSGSTI 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 80 ynpslksrvtsvdktskqfklssvtaadtavyycar 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 60 YNPSSLNDRVFMVSKDQVSLRSLSSVTAADTAVYYCAR 98
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

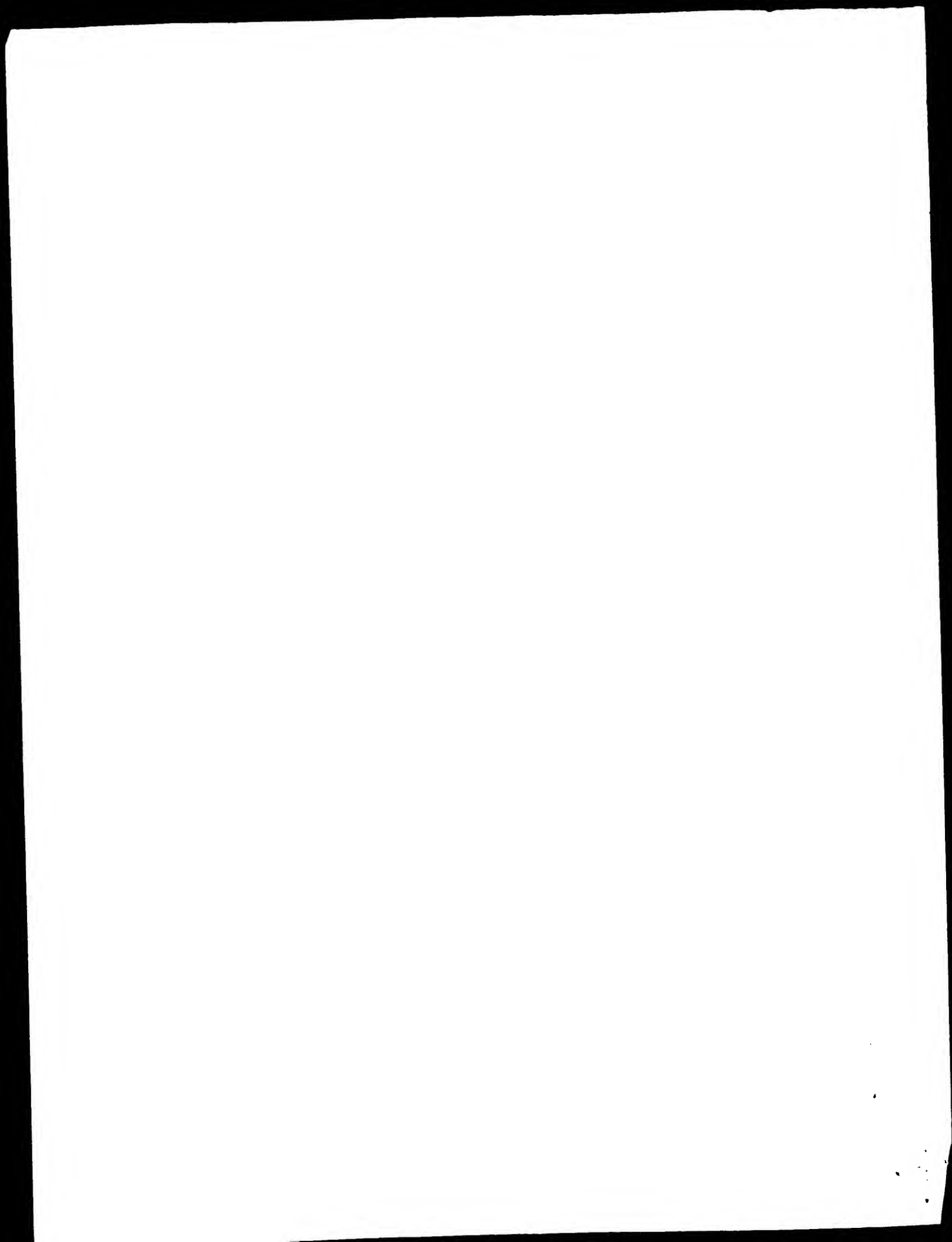
RESULT 15
ID W24536 standard; Protein: 136 AA.
AC W24536;
DE 09-OCT-1997 (first entry)
DE Immunoglobulin B6B7 heavy chain variable region.

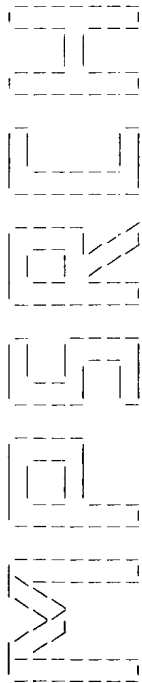
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KW Immunoglobulin: variable region; heavy chain; thyrotropin receptor;
 KW thyroid stimulating activity; light chain; Basedow's disease; antibody;
 KW peripheral blood lymphocyte.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "signal peptide"
 FT Protein 20..136
 PN J09140386-A.
 PD 03-JUN-1997.
 PF 22-NOV-1995; 328235.
 PR 22-NOV-1995; JF-328235.
 PA (EIKE) EIKEN KAGAKU KK.
 DR WPI: 97-344899/32.
 DR N-PSDB: T79919.
 PT Antibody containing immunoglobulin heavy chain mutation - with
 PT thyroid function stimulating activity
 PS Claim 31; Page 14-15; 18pp; Japanese.
 CC W24536-W24539 represent the immunoglobulin heavy and light chain variable
 CC regions isolated from peripheral blood lymphocyte strains. These
 CC sequences were isolated from the B6B7 and 101-2 strains of peripheral
 CC blood lymphocytes of a Basedow's disease patient. These sequences are
 CC replaced, deleted or inserted into an antibody, to create the antibodies
 CC of the invention. The antibodies of the invention have thyroid function
 CC stimulating activity, and act by combining with thyrotropin receptor. The
 CC antibody can be used in a method to detect autoantibodies which have
 CC thyroid function stimulating activity.
 SQ Sequence 136 AA.

Query Match 59.2%; Score 549; DB 22; Length 136;
 Best Local Similarity 69.2%; Pred. No. 1.14e-31;
 Matches 83; Conservative 12; Mismatches 22; Indels 3; Gaps 3;
 Db 20 qvalqesqglvxpsetlsiltctvsqdsi-ssyyvswirppgkglewlgvhyhsqstny 78
 QY :|||||
 1 EVOLLESGGLVKNPSSGTLCTVSGGSLRSSHWSWVPPGKLEWIGVFFSGSTIY 60
 Db 79 nsslskervtsvdtksnqfslkssvtaadtavyyicaree-rgql-rdfaygmdvwdqgt 136
 QY :|||
 61 NPSLNDRVFMVSKDKQVSLSSVTAADTAVYYCARSPKMKNGRMMLDAFDIWGGGT 120

Search completed: Tue Feb 24 07:15:06 1998
 Job time : 31 secs.





(TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on Tue Feb 24 07:11:04 1998; MasPar time 7.28 seconds
361 213 Million cell updates/sec
Tabular output not generated.

Title: >US-08-844-215-5
Description: (1-124) from US08844215.pep
Perfect Score: 926
Sequence: 1 EVOLLEGGGSGVQPGPSLPL IKRYVLENNGGTILVTYSS 124

Scoring table: PAM 150
Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2 part2 3 part3 4 part4 5 part5 6 part6 7 part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 42.049; Variance 78.185; scale 0.538

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	700	75.6	122	5	HV3G_HUMAN IG HEAVY CHAIN V-III	2.75e-124
2	679	73.3	121	5	HV3J_HUMAN IG HEAVY CHAIN V-III	1.15e-119
3	676	73.0	122	5	HV3H_HUMAN IG HEAVY CHAIN V-III	5.23e-119
4	669	72.2	126	5	HV3K_HUMAN IG HEAVY CHAIN V-III	1.80e-117
5	636	68.7	119	5	HV3I_HUMAN IG HEAVY CHAIN V-III	3.09e-110
6	610	65.9	119	5	HV3L_HUMAN IG HEAVY CHAIN V-III	1.49e-102
7	598	64.6	117	5	HV3C_HUMAN IG HEAVY CHAIN P-III	6.16e-102
8	593	64.0	120	5	HV3E_HUMAN IG HEAVY CHAIN V-III	7.57e-101
9	588	63.5	120	5	HV3U_HUMAN IG HEAVY CHAIN V-III	9.28e-100
10	584	63.1	122	5	HV3A_HUMAN IG HEAVY CHAIN V-III	6.80e-99
11	577	62.3	126	5	HV3L_MOUSE IG HEAVY CHAIN P-III	2.26e-97
12	575	62.1	119	5	HV3N_HUMAN IG HEAVY CHAIN V-III	6.23e-97
13	570	61.6	116	5	HV3T_HUMAN IG HEAVY CHAIN V-III	7.60e-96
14	563	60.8	114	5	HV3M_HUMAN IG HEAVY CHAIN V-III	2.51e-94
15	554	59.8	115	5	HV3P_HUMAN IG HEAVY CHAIN V-III	2.25e-92
16	553	59.7	115	5	HV3D_HUMAN IG HEAVY CHAIN V-III	3.70e-92
17	551	59.5	116	5	HV3Q_HUMAN IG HEAVY CHAIN P-III	1.00e-91
18	546	59.0	119	5	HV3P_HUMAN IG HEAVY CHAIN V-III	1.21e-90
19	546	59.0	142	5	HV3I_PAT IG HEAVY CHAIN P-III	1.21e-90
20	543	58.6	114	5	HV3E_HUMAN IG HEAVY CHAIN V-III	5.41e-90
21	542	58.5	123	5	HV3S_MOUSE IG HEAVY CHAIN V-III	8.91e-90
22	542	58.5	123	5	HV3T_MOUSE IG HEAVY CHAIN V-III	8.91e-90

22	542	59.5	123	5	HV3S_MOUSE IG HEAVY CHAIN V-III	8.91e-90
24	539	59.2	123	5	HV3T_MOUSE IG HEAVY CHAIN V-III	8.91e-90
25	538	59.1	117	5	HV3Q_HUMAN IG HEAVY CHAIN V-III	6.53e-89
26	536	57.9	97	5	HV5G_MOUSE IG HEAVY CHAIN V-III	1.77e-88
27	535	57.9	122	5	HV2Q_MOUSE IG HEAVY CHAIN V-III	1.77e-88
28	531	57.3	117	5	HV3Q_HUMAN IG HEAVY CHAIN V-III	2.12e-87
29	531	57.3	123	5	HV2Q_MOUSE IG HEAVY CHAIN V-III	2.12e-87
30	530	57.2	117	5	HV5S_MOUSE IG HEAVY CHAIN P-III	3.49e-87
31	530	57.2	123	5	HV2Q_MOUSE IG HEAVY CHAIN V-III	3.49e-87
32	527	56.9	122	5	HV2Q_MOUSE IG HEAVY CHAIN P-III	1.55e-86
33	526	56.8	117	5	HV5G_MOUSE IG HEAVY CHAIN P-III	2.55e-86
34	526	56.8	144	5	HV2Q_MOUSE IG HEAVY CHAIN P-III	2.55e-86
35	525	56.7	98	5	HV57_MOUSE IG HEAVY CHAIN P-III	4.19e-86
36	520	56.2	117	5	HV3L_MOUSE IG HEAVY CHAIN P-III	5.02e-85
37	519	56.0	144	5	HV3L_MOUSE IG HEAVY CHAIN P-III	8.25e-85
38	516	55.7	117	5	HV3L_MOUSE IG HEAVY CHAIN P-III	3.66e-84
39	514	55.5	119	5	HV3L_MOUSE IG HEAVY CHAIN V-III	9.86e-84
40	512	55.3	113	5	HV34_MOUSE IG HEAVY CHAIN V-III	2.66e-83
41	511	55.2	117	5	HV58_MOUSE IG HEAVY CHAIN P-III	4.36e-83
42	510	55.1	119	5	HV37_MOUSE IG HEAVY CHAIN V-III	7.16e-83
43	506	54.6	119	5	HV4Q_MOUSE IG HEAVY CHAIN V-III	5.20e-82
44	502	54.2	117	5	HV59_MOUSE IG HEAVY CHAIN P-III	3.77e-81
45	501	54.1	115	5	HV32_MOUSE IG HEAVY CHAIN V-III	6.18e-81

ALIGNMENTS

RESULT	1	STANDARD	PRT	122 AA.
ID	HV3G_HUMAN			
AC	P01768;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DE	IG HEAVY CHAIN V-III REGION (CAM).			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES			
PN	[1]			
PP	SEQUENCE			
RX	MEDLINE: 81013459			
FA	LEHMAN D.W., PUTNAM F.W.;			
FI	PROC. NATL. ACAD. SCI. U.S.A. 77:3230-3243(1980).			
CC	- THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A PATIENT WITH			
CC	MACROGLOBULINEMIA			
DR	PIR; A02051; M3HUAM.			
DP	HSSP; P01607; 2FGW.			
KW	IMMUNOGLOBULIN V REGION.			
FT	MOD_RES			
FT	NON_TER			
SQ	SEQUENCE			
Query Match	76.6%	Score 700	DP 5	Length 120.
Best Local Similarity	69.6%	Pred. No. 2.75e-124		
Matches	87	Conservative	26	Mismatches 8
				Indels 4
				Gaps 3
Db	1	qvelsgggvzpgpslrllscasgftfsnyamhwrrppgkglewawvisybbkky 60		
Qy	1	EVALLSGGGVWQPGPSLSLSCASGFTFSAYGMHWVPAPGKGLEWAWISYBBK 60		
Db	61	absckrftisrdsbshlylgrasraetarrfygcardrplyggyra--fnywqgql 117		
Qy	61	STGVKFFTVSPNSPNTPLFANNEPFDUTAVVYCATV--VLFGSIKRYVLENNGG 119		
Db	118	vtvss 122		
Qy	120	VTYSS 124		
RESULT	2	STANDARD	PRT	121 AA.
ID	HV3I_HUMAN			
AC	P01771;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			

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RESULT 4
ID HV3K_HUMAN STANDARD: PRT: 126 AA.
AC P01772; 1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (KOL).
DT
ID
DE
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUtheria; PRIMATES.
RN
RN SEQUENCE, AND DISULFIDE BONDS.
RN MEDLINE; 83289131.
RA MARCUKAT M.; DEISENHOFFER J.; HURFF P.; PALM W.;
RA SCHMIDT W.E.; JUNG H.-D.; PALM W.; HILSCHMANN N.;
RA HOPPE-SEYLER S.Z. PHYSIOL. CHEM. 364:713-747(1983).
RL
RL
[2]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RN MEDLINE; 81072295.
RA MARCUKAT M.; DEISENHOFFER J.; HURFF P.; PALM W.;
RA J. MOL. BIOL. 141:369-391(1980).
DR PIR; A02055; GIHUKL.
DR PDB; 2F84; 12-JUL-89.
DR FDB; 21C2; 12-JUL-89.
DR IMMUNOGLOBULIN V REGION; 3D-STRUCTURE.
KW PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT DISULFID 22 96
FT DISULFID 105 110
FT NON_TER 126 126
FT STRAND 3 7
FT STRAND 11 12
FT STRAND 14 15
FT TURN 14 15
FT STRAND 18 25
FT STRAND 29 31
FT HELIX 34 39
FT STRAND 41 42
FT TURN 46 51
FT STRAND 53 54
FT TURN 58 60
FT TURN 62 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 113
FT STRAND 120 124
FT STRAND 126 AA, 13718 MW, 147,000 P.I. 7.2;
SQ SEQUENCE 126 AA, 13718 MW, 147,000 P.I. 7.2;

Query Match 72.2%; Score 669; DB 5; Length 126;
Best Local Similarity 71.4%; Pred. No. 1,80e-117;
Matches 99, Conservative 17; Mismatches 17; Indels 22;

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Qy 1 EYOLLESGGVVVQPSRLKLSAASGTFISYNGMHWFOAPGKSEWVAITWTFPS
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Db 61 adsvkgrftlsrdnsknllfqmidsrptqvyfcarduhufcssasctdpydy
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Qy 61 SDSVKGRFTVSPNSKNTLFQMSLRPEPTAVYVCATEVLFG-SIKGRYY-LENA
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Db 121 pvtvss 126
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Qy 119 LVTvss 124

RESULT 5
ID HV3L_HUMAN STANDARD: PRT: 119 AA.
AC P01770;

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QY 1 EVOLLESGGVVQPGSLRLSLCAASGFTFSAYGMHWWPQAPKGLWVAGIWDGSGNQY 60
 Db 77 advtkrftisrdnphkntflqmtslrsedtamyyar---wqy--pyyamdwygsgts 131
 QY 61 SDSVKGPFVTSRNSPNTFLQMSLPPDTAVVYCAVEVLFSGIKGPIY-LENWGGGIL 119
 Db 132 vtvs 136
 QY 120 TVSS 124
 RESULT 12
 ID HV3M_HUMAN STANDARD: PRT: 119 AA.
 AC P01775;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG HEAVY CHAIN V-III REGION (LAY).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 75046755.
 RA CAPRA J.D., KEOHE J.M.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 71:4032-4036(1974).
 CC -1- THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN
 CC ACTIVITY.
 DR PIR; A02058; M3HUPM.
 DR HSSP; P01772; 1FGV.
 KW IMMUNOGLOBULIN V REGION.
 FT NON_TER 119 119
 SQ SEQUENCE 119 AA; 12858 MW; 1CEG116C CRC32;

Query Match 62.1%; Score 575; DB 5; Length 119;
 Best Local Similarity 63.9%; Pred. No. 6 23e-q7;
 Matches 78; Conservative 25; Mismatches 13; Indels 6; Gaps 4.
 Db 2 vqllesggglvqpgslrlscaasgftfsasmswvraqpgkglewva--wkyengndkh 59
 QY 2 VQLLESGGVVQPGSLRLSLCAASGFTFSAYGMHWWPQAPKGLWVAGIWF-DGSGNQY 59
 Db 60 yadsvngvrfisrdnphkntflqmgldqzvsaiyycarda--qpyvsptffahwggtl 117
 QY 60 YDSVKGPFVTSRNSPNTFLQMSLPPDTAVVYCAVEVLFSGIKGPIY-LENWGGGIL 119
 Db 118 vt 119
 QY 120 VT 121

RESULT 13
 ID HV3T_HUMAN STANDARD: PRT: 116 AA.
 AC P01781;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG HEAVY CHAIN V-III REGION (GAL).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 75059123.
 RA WATANABE S., BARNIKOL H.U., HORN J., BERTRAM T., HILSCHMANN N.;
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 354:1505-1509(1973).
 RN [2]
 RP REVISION TO THE COMPOSITION OF 28-33.
 RA HILSCHMANN N.;
 RL SUBMITTED (JUN-1975) TO THE PIR DATA BANK.
 CC -1- THIS MJ CHAIN WAS ISOLATED FROM A WALDFNSTROM'S MACROGLOBULIN
 DR PIR; A02064; M3HUGL.
 DR HSSP; P01607; 1FGV.

KW IMMUNOGLOBULIN V REGION.
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 12730 MW; F112826C CRC32;
 Query Match 61.6%; Score 570; DB 5; Length 116;
 Best Local Similarity 70.2%; Pred. No. 7 60e-96;
 Matches 87; Conservative 14; Mismatches 15; Indels 8; Gaps 3;
 Db 1 exqlvesggdlvqpgslrlscaasgfbfblgtwrrqapkgkglewvanik-bgszby 60
 QY 1 EVOLLESGGVVQPGSLRLSLCAASGFTFSAYGMHWWPQAPKGLWVAGIWF-DGSGNQY 60
 Db 61 vdsvkgrftisrdnphkntflqmslrsedtamyyar--wqy--gdy---wqggtlv 112
 QY 61 SDSVKGPFVTSRNSPNTFLQMSLPPDTAVVYCAVEVLFSGIKGPIY-LENWGGGIL 120
 Db 113 tvst 116
 QY 121 TVSS 124
 RESULT 14
 ID HV3M_HUMAN STANDARD: PRT: 119 AA
 AC P01774;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG HEAVY CHAIN V-III REGION (POM).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 75046755.
 RA CAPRA J.D., KEOHE J.M.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 71:4032-4036(1974).
 CC -1- THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN
 CC ACTIVITY.
 DR PIR; A02057; M3HUPM.
 DR HSSP; P01772; 1FGV.
 KW IMMUNOGLOBULIN V REGION.
 FT VARIANT 54 54 N -> D (PROBABLY DUE TO DEAMINATION
 FT NON_TER 119 119 DURING ISOLATION).
 SQ SEQUENCE 119 AA; 12953 MW; 2A5697C2 CRC32;
 Query Match 60.8%; Score 563; DB 5; Length 119;
 Best Local Similarity 63.4%; Pred. No. 2 51e-94;
 Matches 78; Conservative 25; Mismatches 14; Indels 6; Gaps 4.
 Db 1 evqllesggglvqpgslrlscaasgftfsasmswvraqpgkglewva--wkyengndk 58
 QY 1 EVOLLESGGVVQPGSLRLSLCAASGFTFSAYGMHWWPQAPKGLWVAGIWF-DGSGNQ 58
 Db 59 hyadsvngvrfisrdnphkntflqmslrsedtamyyar--qpyvsptffahwggtl 116
 QY 59 YDSVKGPFVTSRNSPNTFLQMSLPPDTAVVYCAVEVLFSGIKGPIY-LENWGGGIL 118
 Db 117 lvt 119
 QY 119 LVT 121
 RESULT 15
 ID HV3E_HUMAN STANDARD: PRT: 115 AA.
 AC P01767;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG HEAVY CHAIN V-III REGION (BUT).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.

US-08-844-215-5.rsp

Thu Feb 26 07:06:09 1998

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RN  SEQUENCE.
RP  MEDLINE: 78137069.
RX  TORANO A.; PUTNAM F.W.;
RA  PROC. NATL. ACAD. SCI. U.S.A. 75:966-969(1978).
FL  -I- THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C REGION OF THIS
CC  CC - MYELOMA PROTEIN IS ALSO GIVEN.
CC  PIR: A02050; A2HUBU.
DR  HSP: P01772; IFGV.
DR  IMMUNOGLOBULIN V REGION.
KW  NON_TER 115 115
FT  SEQUENCE 115 AA: 12379 MW: 90803472 CRC32:
SQ

Query Match 59.8%; Score 554; DB 5; Length 115;
Best Local Similarity 69.0%; Pred. No. 2.25e-92; Indels 1; Gaps 1;
Matches 69; Conservative 21; Mismatches 9;

Db 1 evqlvetggliqpggslrlscaasgftvsbshmswvraqpgkalzwsai-yrggttyy 59
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 EVQLLESGGAVQPGRLSLRLSCAASGFTFSAYGMHWRQAPCKGLEWVAGIWFQGSNOYY 60
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 adsvkgrftisrddsbtyvlqmbslraedtavvyvcardl 99
   :|||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 SDSVKGRFTVSRDNRNLTFLQMSLRPEDTAVYICATIEV 100
   :|||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Search completed: Tue Feb 24 07:11:14 1998
Job time : 10 secs.

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RESULT 2
ENTRY   #type complete
TITLE   Ig heavy chain V region (VH3DJH4) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change
        16-Aug-1996

ACCESSIONS
REFERENCE #authors Marks, J.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.;
          Griffiths, A.D.; Winter, G.
#journal J. Mol. Biol. (1991) 222:581-597
#title By-passing immunization: Human antibodies from V-gene
        libraries displayed on phage.
#cross-references MUID:92085276
#accession S19666
#molecule_type mRNA
#residues 1-121 ##label MAP
#cross-references EMBL:X61646
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98 #domain immunoglobulin homology #label IMM
SUMMARY #length 121 #molecular_weight 13296 #checksum 9195

Query Match 77.8%; Score 720; DB 7; Length 121;
Best Local Similarity 79.0%; Pred. No. 3,32e-78;
Matches 98; Conservative 14; Mismatches 9; Indels 3; Gaps 3;

Db 1 qvqlvesgqgvvqgrslriscasqgftfssygmhwvraqpdkglewvavisdgskyy 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGGCVVQPGKSLRLSQAASGFTFSAYGMHWVRAQPGKLEWVAVIGDGSNYY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 adsvkgrftisrdnsknltlylqmslraedtavyycaetg-vysgwg-yf-dywgqgtlv 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGRFTVSRDNRSLTLFLQMSLRPEDTAVYYCATEVLFSGIKGRYYLENWGQGLTV 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 118 tvss 121
   ||||
QY 121 TVSS 124

RESULT 3
ENTRY   #type complete
TITLE   Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
        16-Aug-1996

ACCESSIONS
REFERENCE #authors Mahmoodi, M.; Edwards, J.; Cairns, E.; Bell, D.
          #submission Submitted to the EMBL Data Library, October 1994
          #description Molecular characterization of natural human anti-Sm
          autoantibodies.
#accession S48797
#status preliminary
#molecule_type mRNA
#residues 1-128 ##label MAH
#cross-references EMBL:246379
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98 #domain immunoglobulin homology #label IMM
SUMMARY #length 128 #molecular_weight 14474 #checksum 9058

Query Match 77.6%; Score 719; DB 7; Length 128;
Best Local Similarity 77.3%; Pred. No. 5,10e-78;
Matches 99; Conservative 13; Mismatches 12; Indels 4; Gaps 1;

Db 1 qvqlvesgqgvvqgrslriscasqgftfssygmhwvraqpdkglewvavisdgskyy 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGGCVVQPGKSLRLSQAASGFTFSAYGMHWVRAQPGKLEWVAVIFDGSNYY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 adsvkgrftisrdnsknltlylqmslraedtavyycaetg-vysgwg-yf-dywgqgtlv 119
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGRFTVSRDNRSLTLFLQMSLRPEDTAVYYCATEVLFSGIKGRYYLENWGQGLTV 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 120 tvss 123
   ||||
QY 121 TVSS 124

RESULT 5
ENTRY   #type complete
TITLE   Ig heavy chain V region (M72) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change
        16-Aug-1996

ACCESSIONS
REFERENCE #authors Schroeder Jr., H.W.; Wang, J.Y.
          #journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6146-6150
          #title Preferential utilization of conserved immunoglobulin heavy
          chain variable gene segments during human fetal life.
#cross-references MUID:90349571
#accession E36005
#status preliminary
#molecule_type mRNA
#residues 1-122 ##label SCH

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##cross-references GB:M34030
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98 #domain immunoglobulin homology #label IMM
SUMMARY
#length 122 #molecular weight 13527 #checks 630

Query Match 76.9%; Score 704; DB 7; Length 122;
Best Local Similarity 77.6%; Pred. No. 5.51e-76;
Matches 97; Conservative 15; Mismatches 8; Indels 4; Gaps 3;

Db 1 qvlgvesggvvgpgrslrlscaasgftfssygmhwrqapqgkglewvavisdgskyy 60
QY 1 EVQLLESGGVGVPGRSLRLSCAASGFTFSAYGMHWRQAPQKGLEWVAVISDGSNYY 60

Db 61 adsvkgrftisrdnsksntlylqmslraedavvycaedr-hse--swygmndvwaqgtt 117
QY 61 SDSVKGRFTVSRNSPNTFLQWNSLPETAVVYCAETEVLFSIKSPYY-LENWQVQJTL 119

Db 118 tvss 122
QY 120 TVSS 124

RESULT 6
ENTRY #type complete
TITLE Ig heavy chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change
16-Aug-1996
ACCESSIONS S31603
REFERENCE S31585
#authors Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.;
Tonnelie, C.
#submission submitted to the EMBL Data Library, June 1992
#description Mechanisms that generate human immunoglobulin diversity
operate from the 8th week of gestation in fetal liver.
#accession S31603
#status preliminary
#molecule_type mRNA
#residues 1-132 #label CUI
##cross-references EMBL:Z14168
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
30-113 #domain immunoglobulin homology #label IMM
SUMMARY
#length 132 #molecular weight 14696 #checks 8700

Query Match 75.9%; Score 703; DB 7; Length 132;
Best Local Similarity 79.8%; Pred. No. 7.53e-76;
Matches 99; Conservative 13; Mismatches 5; Indels 7; Gaps 2;

Db 16 qvlgvesggvvgpgrslrlscaasgftfssygmhwrqapqgkglewvavisdgskyy 75
QY 1 EVQLLESGGVGVPGRSLRLSCAASGFTFSAYGMHWRQAPQKGLEWVAVISDGSNYY 60

Db 76 adsvkgrftisrdnsksntlylqmslraedavvycaekd-iff-----yyfdywgsgtlv 128
QY 61 SDSVKGRFTVSRNSPNTFLQWNSLPETAVVYCAETEVLFSIKSPYYLENWQVQJTLV 120

Db 129 tvss 132
QY 121 TVSS 124

RESULT 7
ENTRY #type complete
TITLE Ig heavy chain V-III region (Cam) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Aug-1990 #sequence_revision 23-Oct-1981 #text_change
31-Mar-1997
ACCESSIONS A02051
REFERENCE A02051

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#authors Lehman, D.W.; Putnam, F.W.
#journal Proc. Natl. Acad. Sci. U.S.A. (1980) 77:3239-3243
#title Amino acid sequence of the variable region of a human mu
chain: location of a possible J-H segment.
#cross-references MUID:81013859
#accession A02051
#molecule_type protein
#residues 1-122 #label LEH
COMMENT This mu chain was isolated from the plasma of a patient with
macroglubulinemia.
GENETICS
#gene GDB:IGHV@
#map_position 14q22.33-14q22.33
#cross-references QDB:128528
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin; pyroglutamic acid
FEATURE
15-98 #domain immunoglobulin homology #label IMM
1 #modified site pyrrolidone carboxylic acid (Gln) #status
experimental
22-96 #disulfide_bonds #status predicted
SUMMARY #length 122 #molecular weight 13668 #checks 7281

Query Match 75.6%; Score 700; DB 2; Length 122;
Best Local Similarity 69.6%; Pred. No. 1.92e-75;
Matches 87; Conservative 26; Mismatches 8; Indels 4; Gaps 3;

Db 1 qvlgvesggvvgpgrslrlscaasgftfssygmhwrqapqgkglewvavisdgskyy 60
QY 1 EVQLLESGGVGVPGRSLRLSCAASGFTFSAYGMHWRQAPQKGLEWVAVISDGSNYY 50

Db 61 adsvkgrftisrdnsksntlylqmslraedavvycaedrplygbyra--f-pywgagtl 117
QY 61 SDSVKGRFTVSRNSPNTFLQWNSLPETAVVYCAETE-VLPFSIKSPYYLENWQVQJTL 119

Db 118 tvss 122
QY 120 TVSS 124

RESULT 8
ENTRY #type fragment
TITLE Ig heavy chain V region - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
16-Aug-1996
ACCESSIONS S31674
REFERENCE S31585
#authors Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.;
Tonnelie, C.
#submission submitted to the EMBL Data Library, June 1992
#description Mechanisms that generate human immunoglobulin diversity
operate from the 8th week of gestation in fetal liver.
#accession S31674
#status preliminary
#molecule_type mRNA
#residues 1-139 #label CUI
#cross-references EMBL:Z14204
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
34-117 #domain immunoglobulin homology #label IMM
SUMMARY #length 139 #checks 3756

Query Match 75.2%; Score 696; DB 7; Length 139;
Best Local Similarity 78.2%; Pred. No. 6.68e-75;
Matches 97; Conservative 14; Mismatches 9; Indels 4; Gaps 3;

Db 20 qvlgvesggvvgpgrslrlscaasgftfssygmhwrqapqgkglewvavisdgskyy 79
QY 1 EVQLLESGGVGVPGRSLRLSCAASGFTFSAYGMHWRQAPQKGLEWVAVISDGSNYY 60

Db 80 adsvkgrftisrdnsksntlylqmslraedavvycaekd-iff-wf--dpwgagtlv 135

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US-08-844-215-5.rpr

Thu Feb 26 07:06:08 1998

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QY 61 SDSVKGRTVSRDNRNTLFLQMSLRPEDTAVYYCATEVLFSGIKGRYYLENWGQGTILV 120
Db 136 tvss 139
QY 121 TVSS 124

RESULT 9
ENTRY S31112 #type complete
TITLE Ig heavy chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Dec-1993 #sequence_revision 26-May-1995 #text_change
16-Aug-1996
ACCESSIONS S31112
REFERENCE Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol,
#authors M.J.D.; Vossen, J.M.; Schuurman, R.K.B.
#journal Eur. J. Immunol. (1992) 22:247-251
#title Restricted utilization of germ-line V(H)3 genes and short
diverse third complementarity-determining regions (CDR3) in
human fetal B lymphocyte immunoglobulin heavy chain
rearrangements.
#accession S31112 preliminary; nucleic acid sequence not shown;
#status translation not shown
#molecule_type mRNA
#residues 1-120 #label RAA
#cross-references EMBL:X62961
#note the nucleotide sequence was submitted to the EMBL Data
Library, October 1991
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 15-98
SUMMARY #domain immunoglobulin homology #label IMM
#length 120 #molecular_weight 12778 #checksum 4374

Query Match 74.8%; Score 693; DB 7; Length 118;
Best Local Similarity 79.0%; Pred. No. 1.70e-74;
Matches 98; Conservative 15; Mismatches 5; Indels 6; Gaps 3;

Db 1 qvqlvesggvvqpqrslrlscasgfftsygmhvrqapqkglewvavisydgsnkyy 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLESGGGVVPGRSLRLSCAASGFTFSAYGMHVRQAPGKLEWVAGLWFDGNSQYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 adsvkgrftisrdnsknltlylqmslraedtavyycatd---gg-kaaf---diwqgqtlv 114
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGRTVSRDNRNTLFLQMSLRPEDTAVYYCATEVLFSGIKGRYYLENWGQGTILV 120
Db 115 tvss 118
:|||||
QY 121 TVSS 124

RESULT 11
ENTRY S36278 #type fragment
TITLE Ig heavy chain V region (clone alpha-THY-23) - human
(fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
16-Aug-1996
ACCESSIONS S36278
REFERENCE Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.;
#authors Emberton, M.J.; McCafferty, J.; Baier, M.; Holliger, K.P.;
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
G.
#journal EMBO J. (1993) 12:725-734
#title Human anti-self antibodies with high specificity from phage
display libraries.
#accession S36278
#status preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-120 #label GRI
#cross-references EMBL:Z18830
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 15-98
SUMMARY #domain immunoglobulin homology #label IMM
#length 120 #checksum 7337

Query Match 74.5%; Score 690; DB 7; Length 120;
Best Local Similarity 73.2%; Pred. No. 4.33e-74;
Matches 90; Conservative 18; Mismatches 12; Indels 3; Gaps 4;

Db 1 qvqlqsgggvvqpqrslrlscasgfftsygmhvrqapqkglewvavisydgsnkyy 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLESGGGVVPGRSLRLSCAASGFTFSAYGMHVRQAPGKLEWVAGLWFDGNSQYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 adsvkgrftisrdnsknltlylqmslraedtavyycatd---vv-aryl---dywqgqtlv 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGRTVSRDNRNTLFLQMSLRPEDTAVYYCATEVLFSGIKGRYYLENWGQGTILV 120
Db 118 tvs 120
:|||||
QY 121 TVS 123

RESULT 12
ENTRY S69910 #type complete

```

```

TITLE      Ig V-D-J region (KR) - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
          09-May-1997
ACCESSIONS S69910
REFERENCE   S69909
#authors   Sahota, S.; Hamblin, T.; Osier, D.G.; Stevenson, F.K.
#journal    Leukemia (1994) 8:1285-1289
#title      Assessment of the role of clonogenic B lymphocytes in the
           pathogenesis of multiple myeloma.
#accession S69910
##status   preliminary; nucleic acid sequence not shown
##molecule_type mRNA
##residues 1-122 ##label SAH
##cross-references EMBL:Z33400
##note      the sequence of residues 108-122 and the corresponding
           nucleic acid sequence are not shown
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY        #length 122 #molecular-weight 13511 #checksum 583

Query Match      74.4% Score 689; DB 7; Length 122;
Best Local Similarity 75.2%; Pred. No. 5.92e-74;
Matches 94; Conservative 15; Mismatches 12; Indels 4; Gaps 4;

Db 1 qvqlvesggvqpqsrllscsttsftfssghmhvrrqapkgkglwrravysdgsnkyy 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGGVPQPGPSLPFLSCAASGFTPSAYGMHWVPAPGKGLWVAGIWFDSNYY 60

Db 61 adsvtrfisdnskntlylgnmslraedtavvycaedrkw--gwaltdywgqgtlv 117
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGPFTVSPNSPTLFLMNSLPPTTAVVYCA-TEVLFSGIKRYPYLENWQGGTIV 119

Db 118 vtvs 122
   |||||
QY 120 TVSS 124

RESULT 13
ENTRY     G36005 #type complete
TITLE     Ig heavy chain V region (M74) - human
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change
          16-Aug-1996
ACCESSIONS G36005
REFERENCE   A36005
#authors   Schroeder Jr., H.W.; Wang, J.Y.
#journal    Proc Natl Acad Sci U S A (1990) 87:6146-6150
#title      Preferential utilization of conserved immunoglobulin heavy
           chain variable gene segments during human fetal life.
#cross-references MIM:190344571
#accession G36005
##status   preliminary
##molecule_type mRNA
##residues 1-121 ##label SCH
##cross-references GB:M34031
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE       15-98
SUMMARY        #length 121 #molecular-weight 13508 #checksum 6962

Query Match      74.3% Score 688; DB 7; Length 121;
Best Local Similarity 77.4%; Pred. No. 8.08e-74;
Matches 96; Conservative 14; Mismatches 11; Indels 2; Gaps 3;

Db 1 qvqlvesggvqpqsrllscsttsftfssghmhvrrqapkgkglwrravysdgsnkyy 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGGVPQPGPSLPFLSCAASGFTPSAYGMHWVPAPGKGLWVAGIWFDSNYY 60

Db 61 adsvtrfisdnskntlylgnmslraedtavvycaedrkw--gwaltdywgqgtlv 117
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGPFTVSPNSPTLFLMNSLPPTTAVVYCA-TEVLFSGIKRYPYLENWQGGTIV 120

Db 118 vtvs 121
   |||||
QY 121 TVSS 124

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Db 118 tvss 121
   |||||
QY 121 TVSS 124

RESULT 14
ENTRY     S31598 #type complete
TITLE     Ig heavy chain V region - human
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
          16-Aug-1996
ACCESSIONS S31598
REFERENCE   S31585
#authors   Collier, A.M.; Gauthier, L.; Roublil, L.; Fougereau, M.;
           Tonnelie, C.
#submission submitted to the EMBL Data Library, June 1992
#description Mechanisms that generate human immunoglobulin diversity
           operate from the 8th week of gestation in fetal liver
#accession S31598
##status   preliminary
##molecule_type mRNA
##residues 1-135 ##label CUI
##cross-references EMBL:Z14170
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE       31-114
SUMMARY        #domain immunoglobulin homology #label IMM
           #length 135 #molecular-weight 14957 #checksum 4425

Query Match      74.3% Score 688; DB 7; Length 135;
Best Local Similarity 77.4%; Pred. No. 8.08e-74;
Matches 96; Conservative 15; Mismatches 8; Indels 5; Gaps 4;

Db 17 qvqlvesggvqpqsrllscsttsftfssghmhvrrqapkgkglwrravysdgsnkyy 76
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGGVPQPGPSLPFLSCAASGFTPSAYGMHWVPAPGKGLWVAGIWFDSNYY 60

Db 77 adsvtrfisdnskntlylgnmslraedtavvycaedrkw--gwaltdywgqgtlv 131
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGPFTVSPNSPTLFLMNSLPPTTAVVYCA-TEVLFSGIKRYPYLENWQGGTIV 120

Db 132 tvss 135
   |||||
QY 121 TVSS 124

RESULT 15
ENTRY     S31510 #type complete
TITLE     Ig heavy chain - human
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
          16-Aug-1996
ACCESSIONS S31510
REFERENCE   S31509
#authors   Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
#submission submitted to the EMBL Data Library, December 1992
#description Dominance of clonotypic patterns and variable gene usage of
           anti-DNA autoantibodies from patient with lupus.
#accession S31510
##status   preliminary
##molecule_type mRNA
##residues 1-133 ##label CHA
##cross-references EMBL:X69865
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE       25-109
SUMMARY        #domain immunoglobulin homology #label IMM
           #length 133 #molecular-weight 14770 #checksum 9812

Query Match      74.1% Score 686; DB 7; Length 133;
Best Local Similarity 76.4%; Pred. No. 1.51e-73;
Matches 94; Conservative 17; Mismatches 10; Indels 2; Gaps 2;

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US-08-844-215-5.rpr

Thu Feb 26 07:06:08 1998

Db 13 vhlvesggvvparslriscasqftfssfamhwrqapkglewaaaisydnsneyya 72
QY 2 VOLLESGGGVVPGESLRLSCAASGTFFSAYGMHWRQAPCKGLEWVAGIWFDSNQYYS 61
Db 73 dsvkgrftvsrdnsksntlylgmnsraedtaavyycar-vsreaf-vriaftywqhtllt 130
QY 62 DSVKGRFTVSRDNRNTLFLOMNSLRPEDTAVYYCATEVLFSGIKGRYYLENMGQGTLYT 121
Db 131 vss 133
QY 122 VSS 124

Search completed: Tue Feb 24 07:12:14 1998
Job time : 42 secs.

W O R L D

(TM)

Release 2 ID John F. Collins, Biocomputing Research Unit
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Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:30:15 1998. Master time 3:55:30.00
Tabular output not generated. 177,836 Million cell updates/sec

Title: >US-08-844-215-5
Description: (1-124) from US08844215.pep
Perfect Score: 926
Sequence: 1 EVOLLESGGVVQPGSLRL. IKPYYLENWGGTLTVSS 124

Scoring table: PAM 150
Gap 11

Searched: 56402 seqs, 5095871 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:58 10:59
10:PT92 11:PT93 12:PT94 13:PT95 14:PT96

Statistics: Mean 28.178 Variance 148.297 scale 0.190

Pred No is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	695	75.1	119	7	US-08-331- Sequence 45, Applicati	1.07e-45
2	687	74.2	125	7	US-08-478- Sequence 98, Applicati	4.64e-45
3	684	73.9	120	7	US-07-942- Sequence 35, Applicati	8.05e-45
4	683	73.8	141	6	US-08-259- Sequence 2, Applicatio	9.67e-45
5	683	73.8	141	7	US-08-468- Sequence 2, Applicatio	1.16e-44
6	682	73.7	125	11	PCT-US93-1 Sequence 1, Applicati	5.05e-44
7	674	72.8	122	11	PCT-US93-0 Sequence 14, Applicati	7.29e-44
8	672	72.6	122	11	PCT-US93-0 Sequence 12, Applicati	1.05e-43
9	670	72.4	122	11	PCT-US93-0 Sequence 33, Applicati	6.59e-43
10	660	71.3	125	7	US-07-942- Sequence 2, Applicatio	5.59e-43
11	660	71.3	142	6	US-08-305- Sequence 21, Applicati	9.51e-43
12	658	71.1	122	11	PCT-US93-0 Sequence 14, Applicati	1.14e-42
13	657	71.0	113	6	US-08-478- Sequence 141, Applic	1.65e-42
14	655	70.7	116	6	US-08-211- Sequence 6, Applicatio	1.98e-42
15	654	70.6	125	11	PCT-US93-1 Sequence 5, Applicatio	1.94e-42
16	654	70.6	125	11	PCT-US93-1 Sequence 118, Applicat	2.58e-41
17	646	69.8	98	6	US-08-211- Sequence 93, Applicati	2.58e-41
18	640	69.1	117	7	US-07-942- Sequence 70, Applicati	2.58e-41
19	640	69.1	130	7	US-08-478- Sequence 6, Applicati	4.47e-41
20	640	69.1	130	7	US-08-478- Sequence 72, Applicati	4.47e-41
21	637	68.8	119	12	PCT-US94-0 Sequence 72, Applicati	4.47e-41
22	637	68.8	125	13	PCT-US95-0 Sequence 72, Applicati	4.47e-41

22	637	68.8	125	7	US-08-376- Sequence 72, Applicati	4.47e-41
23	634	68.5	125	13	PCT-US95-0 Sequence 74, Applicati	7.75e-41
24	634	68.5	125	7	US-08-276- Sequence 77, Applicati	7.75e-41
25	634	68.5	125	7	US-08-276- Sequence 75, Applicati	7.75e-41
26	634	68.5	125	7	US-08-276- Sequence 74, Applicati	7.75e-41
27	634	68.5	125	7	US-08-276- Sequence 77, Applicati	7.75e-41
28	634	68.5	125	13	PCT-US95-0 Sequence 76, Applicati	7.75e-41
29	634	68.5	125	13	PCT-US95-0 Sequence 2, Applicatio	1.12e-40
30	632	68.3	144	5	US-08-326- Sequence 4, Applicatio	1.12e-40
31	626	67.6	443	14	PCT-US96-1 Sequence 18, Applicati	4.84e-40
32	624	67.4	117	7	US-07-942- Sequence 26, Applicati	5.81e-40
33	623	67.3	232	11	PCT-US93-0 Sequence 75, Applicati	8.38e-40
34	621	67.1	125	7	US-08-376- Sequence 75, Applicati	8.38e-40
35	621	67.1	125	13	PCT-US95-0 Sequence 46, Applicati	1.01e-39
36	620	67.0	113	11	PCT-US93-1 Sequence 22, Applicati	1.01e-39
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38	620	67.0	119	6	US-07-988- Sequence 135, Applicat	1.21e-39
39	619	66.8	123	6	US-08-211- Sequence 73, Applicati	1.45e-39
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42	616	66.5	117	7	US-07-942- Sequence 20, Applicati	2.51e-39
43	615	66.4	120	11	PCT-US93-1 Sequence 95, Applicati	2.51e-39
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45	614	66.3	122	7	US-08-487- Sequence 49, Applicati	3.02e-39

ALIGNMENTS

RESULT 1
ID US-08-331-398A-46 STANDARD: PPT: 119 AA
XX
AC xxxxxx
DT 01-JAN-1900
XX Sequence 46, Application US/08331398A.
DE
CC Sequence 46, Application US/08331398A
CC Patent No. 5608039
CC GENERAL INFORMATION:
CC APPLICANT: Pastan, Ira
CC APPLICANT: Willingham, Mark
CC APPLICANT: Fitzgerald, David
CC APPLICANT: Brinkmann, Ulrich
CC APPLICANT: Pai, Lee
CC TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
CC AND THEIR USES (as amended)
CC NUMBER OF SEQUENCES: 68
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew
CC STREET: One Market Plaza, Steuart Street Plaza
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105-1492
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/331,398A
CC FILING DATE: 28-OCT-1994
CC CLASSIFICATION: 435
CC PRIORITY APPLICATION DATA:
CC FILING DATE: 30-SEP-1991
CC PRIOR APPLICATION NUMBER: US 07/596,289
CC FILING DATE: 12-OCT-1990
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Hunter, Tom
CC REGISTRATION NUMBER: 38,498
CC REPRESENTATIVE NUMBER: 01580-1261100S

CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE: (415) 543-9600	
CC	TELEFAX: (415) 543-5043	
CC	INFORMATION FOR SEQ ID NO: 46:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH: 119 amino acids	
CC	TYPE: amino acid	
CC	STRANDEDNESS:	
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CC	MOLECULE TYPE: protein	
CC	FEATURE:	
CC	NAME/KEY: Protein	
CC	LOCATION: 1..119	
CC	OTHER INFORMATION: /note= "Human fetal immunoglobulin	
CC	OTHER INFORMATION: 56P1/CL Variable Heavy chain (V-H)"	
CC	SEQUENCE 119 AA: 13279 MW: 79818 CN:	
CC	Query Match 75.1%; Score 695; DB 7: Length 119:	
CC	Best Local similarity 78.2%; Pred. No. 1.07e-45; Indels 5. Gaps 2:	
CC	Matches 97; Conservative 14; Mismatches 8;	
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CC	RESULT 2	
CC	ID US-08-478-039-99 STANDARD; PRT: 125 AA.	
CC	XXxxxx	
CC	01-JAN-1900	
CC	DE Sequence 99, Application US/08478039.	
CC	Sequence 99, Application US/08478039	
CC	Patent No. 5681722	
CC	GENERAL INFORMATION:	
CC	APPLICANT: Newman, Roland A.	
CC	APPLICANT: Hanna, Nabil	
CC	APPLICANT: Raab, Ronald W.	
CC	TITLE OF INVENTION: Recombinant Antibodies for Human Therapy	
CC	NUMBER OF SEQUENCES: 114	
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESS: HURNS, DOANE, SWECKER & MATHIS	
CC	STREET: 699 Prince St.	
CC	CITY: Alexandria	
CC	STATE: VA	
CC	COUNTRY: USA	
CC	ZIP: 22313-1404	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: Floppy disk	
CC	COMPUTER: IBM PC compatible	
CC	OPERATING SYSTEM: PC-DOS/MS-DOS	
CC	SOFTWARE: PatentIn Release #1.0, Version #1.30	
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER: US/08/478,039	
CC	FILING DATE: 07-JUN-1995	
CC	CLASSIFICATION: 435	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER: US 08/375,072	
CC	FILING DATE: 25-JAN-1995	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER: US 07/912,292	
CC	FILING DATE: 10-JUL-1992	

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CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 07/066,281  
CC FILING DATE: 23-MAR-1992  
CC PRIOR APPLICATION DATA:  
CC PRIOR APPLICATION NUMBER: US 07/735,064  
CC FILING DATE: 25-JUL-1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Teskin Esq., Robin L.  
CC REGISTRATION NUMBER: 35,030  
CC REFERENCE/DOCKET NUMBER: 012712-160  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 703-836-6620  
CC TELEFAX: 703-836-2021  
CC INFORMATION FOR SEQ ID NO: 99:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 125 amino acids  
CC TYPE: amino acid  
CC STRANDEDNESS: not relevant  
CC TOPOLOGY: not relevant  
CC MOLECULE TYPE: peptide  
CC POSITION IN GENOME:  
CC CHROMOSOME/SEGMENT: 18/2  
CC SEQUENCE: 125 AA, 13543 MW, 93321 CN;  
  
Query Match 74.2%; Score 687; DB 7; Length 125;  
Best Local Similarity 73.8%; Pred No. 4,64e+45;  
Matches 93; Conservative 16; Mismatches 12; Indels 4; Gaps  
  
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Db b1 ADSVKGRFTLSRDSKNLTLYLQMNSLRADETAVYICAKGQWLYYG-SGSVHFMDPWGQQT 114  
Qy 61 SDSVKGRFTVSRDNRNTLYFLQMNSLRPREDTAVYVCAT-EVLFGSIKGRYY-LFNNGQQT 118  
  
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ID US-07-942-245-35  
XX xxxxxx  
DT 01-JAN-1900  
DE Sequence 35, Application US/07942245.  
XX Sequence 35, Application US/07942245  
CC Patent No. 5639641  
CC GENERAL INFORMATION:  
CC APPLICANT: PEDERSEN, Jan T.  
CC APPLICANT: SEARLE, Stephen M.J.  
CC APPLICANT: REES, Anthony R.  
CC APPLICANT: ROGUSKA, Michael A.  
CC APPLICANT: GUILD, Braydon C.  
CC TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF ROBERT  
CC TITLE OF INVENTION: ANTIBODIES  
CC NUMBER OF SEQUENCES: 522  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Sughrue, Lion, Zinn, Macpeak & Sears  
CC STREET: 2100 Pennsylvania Avenue, N.W.  
CC CITY: Washington  
CC STATE: D.C.  
CC COUNTRY: United States  
CC ZIP: 20037-3202  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: HP 9000/700 Workstation  
CC OPERATING SYSTEM: UNIX  
CC SOFTWARE: In house
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CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US 07/943,245
CC FILING DATE: 09-SEP-1992
CC CLASSIFICATION: 530
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (202) 292-7060
CC TELEFAX: (202) 293-7850
CC TELEX: 6491103
CC INFORMATION FOR SEQ ID NO: 35
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 120 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 120 AA, 13421 MW, 78517 CN.

Query Match 73.9%; Score 684; DB 7; Length 120;
Best Local Similarity 77.2%; Pred. No 8,05e-45;
Matches 95; Conservative 14; Mismatches 11; Indels 3; Gaps 2;

Db 1 QVQLVESGGGVVQPGPSLPLSFAASGFTFSVAMHWVQAPKSKLEWVAVISYDSENKYY 60
QY 1 EVQLLESQGVVQPGPSLPLSFAASGFTFSVAMHWVQAPKSKLEWVAVISYDSENKYY 60

Db 61 ADSVKGPFITSDNSKNTLYLQMNLSLRDPAVYVCAPDK-DW-GWAFDYWGQGTLLV 117
QY 61 SDSVKGPFITSDNSKNTLYLQMNLSLRDPAVYVCAPDK-DW-GWAFDYWGQGTLLV 120

Db 118 TVS 120
QY 121 TVS 123

RESULT 4
ID US-08-259-372A-2 STANDARD: PPT: 141 AA
XX xxxxxx
XX 01-JAN-1900
XX Sequence 2, Application US/08259372A
XX Sequence 2, Application US/08259372A
XX Patent No. 5565354
XX GENERAL INFORMATION:
XX APPLICANT: Ostberg, Lars G.
XX TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
XX TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIG
EN
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, Eighth Floor
CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/259,372A
CC FILING DATE: 14-JUN-1994
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/971,426
CC FILING DATE: 21-APR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/976,036
CC FILING DATE: 27-MAR-1991
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/538,796
CC FILING DATE: 15-MAY-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/192,754
CC FILING DATE: 11-MAY-1988
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/925,196
CC FILING DATE: 31-OCT-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/904,517
CC FILING DATE: 05-SEP-1986
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-50-7
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 328-2400
CC TELEFAX: (415) 576-0300
CC INFORMATION FOR SEQ ID NO: 2
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 141 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 141 AA, 15613 MW, 114738 CN.

Query Match 73.8%; Score 683; DB 6; Length 141;
Best Local Similarity 77.6%; Pred. No 9,67e-45;
Matches 97; Conservative 10; Mismatches 14; Indels 4; Gaps 2;

Db 20 QVQLVESGGGVVQPGPSLPLSFAASGFTFSVAMHWVQAPKSKLEWVAVISYDSENKYY 79
QY 1 EVQLLESQGVVQPGPSLPLSFAASGFTFSVAMHWVQAPKSKLEWVAVISYDSENKYY 60

Db 80 ADSVKGPFITSDNSKNTLYLQMNLSLRDPAVYVCAPDK-DW-GWAFDYWGQGTLLV 136
QY 61 SDSVKGPFITSDNSKNTLYLQMNLSLRDPAVYVCAPDK-DW-GWAFDYWGQGTLLV 119

Db 137 TVVSS 141
QY 120 TVVSS 124

RESULT 5
ID US-08-468-671-2 STANDARD: PPT: 141 AA
XX xxxxxx
XX 01-JAN-1900
XX Sequence 2, Application US/08468671
XX Sequence 2, Application US/08468671
XX Patent No. 5648077
XX GENERAL INFORMATION:
XX APPLICANT: Ostberg, Lars G.
XX TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
XX TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIG
EN
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, Eighth Floor
CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/468,671
CC FILING DATE: 14-JUN-1994
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/971,426
CC FILING DATE: 21-APR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/976,036
CC FILING DATE: 27-MAR-1991
CC PRIOR APPLICATION DATA:

US-08-844-215-5.ra1

Thu Feb 26 07:06:06 1998

NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 18/2
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..125

SEQUENCE 125 AA: 13454 MW: 94507 CN:
Query Match 73.7% Score 682; DB 11; Length 125;
Best Local Similarity 73.8% Pred. No. 1.16e-44;
Matches 93; Conservative 18; Mismatches 12; Indels 3; Gaps 4;

Db 1 EVOLVESGGVQPGSPRLSLCAASGFTFSYAMSNVVRQAPGKGLWVSAISGSGSTTY 60
QY 1 EVOLVESGGVQPGSPRLSLCAASGFTFSYAMSNVVRQAPGKGLWVSAISGSGSTTY 60

Db 61 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYCTGGLVYVG-SCSYHMFDPWGGT 119
QY 61 SDSVKGRTISRDNKNTLYLQMSLRAEDTAVYCTGGLVYVG-SCSYHMFDPWGGT 119

Db 120 LVTSS 125
QY 119 LVTSS 124

RESULT 7
ID PCT-US93-08435-43 STANDARD; PRT: 122 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 43, Application PC/TUS9308435.

Sequence 43, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Conferring Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man

APPLICATION NUMBER: US/08/458,671
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/548,796
FILING DATE: 15-JUN-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 141 AA: 15613 MW: 114738 CN;

Query Match 73.8% Score 683; DB 7; Length 141;
Best Local Similarity 77.0% Pred. No. 9.67e-45;
Matches 97; Conservative 10; Mismatches 14; Indels 4; Gaps 2;

Db 20 QVQLVESGGVQPGSPRLSLCAASGFTFSYAMSNVVRQAPGKGLWVSAISGSGSTTY 79
QY 1 EVOLVESGGVQPGSPRLSLCAASGFTFSYAMSNVVRQAPGKGLWVSAISGSGSTTY 60

Db 80 ADSVKGRTISRDNKNTLYLQMSLRAEDTAVYCTGGLVYVG-SCSYHMFDPWGGT 136
QY 61 SDSVKGRTISRDNKNTLYLQMSLRAEDTAVYCTGGLVYVG-SCSYHMFDPWGGT 119

Db 137 VTYSS 141
QY 120 VTYSS 124

RESULT 6
ID PCT-US93-10555-1 STANDARD; PRT: 125 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 1, Application PC/TUS9310555.

Sequence 1, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
ATES
TITLE OF INVENTION: THEREOF

CC NUMBER OF SEQUENCES: 61
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Howson and Howson
 CC STREET: Box 457, 321 Norristown Road
 CC CITY: Spring House
 CC STATE: PA
 CC COUNTRY: USA
 CC ZIP: 19477
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/08435
 CC FILING DATE:
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/941,654
 CC FILING DATE: 09-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Bak, Mary E.
 CC REGISTRATION NUMBER: 31,215
 CC REFERENCE/DOCKET NUMBER: SBC P50107
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (215) 540-9200
 CC TELEFAX: (215) 540-5818
 CC INFORMATION FOR SEQ ID NO. 43:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 122 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 122 AA: 1313 MW: 87403 CN:

Query Match 72.8%; Score 674; DB 11; Length 122;

Best Local Similarity 75.0%; Pred. No. 5,05e-44;

Matches 98; Conservative 14; Mismatches 15; Indels 2; Gaps 2;

Db 1 EVQLLEGGGSLVQPGSSRLKLSCAASGFTFSYAMSVWPAAPGKGLWVAELSDGSKYTY 60
 QY 1 EVQLLEGGGVQVQPRSLFLSCAASGFTFSYAGSMHWVPAAPGKGLWVAGWFGSGNQYY 60
 Db 61 PTVTVGRTPTISDNKNTLYLQMSLRAEDTAVVYCASLIYYG-YDG-YAMDYWGQGTLY 118
 QY 61 SDSVAGRETVPSPDNPSTIFLQMSLPPEDTAVVYCATEVLFPGSKGYYLENWQGTLY 120
 Db 119 TVSS 122
 QY 121 TVSS 124

RESULT 8
 ID PCT-US93-08435-14 STANDARD: PPT: 122 AA.
 XX AC xxxxxx
 XX DT 01-JAN-1900
 XX DE
 XX SE Sequence 14, Application PC/TUS9308435.
 CC Sequence 14, Application PC/TUS9308435
 CC GENERAL INFORMATION:
 CC APPLICANT: SmithKline Beecham, Corporation
 CC APPLICANT: U. S. Government, Secretary of
 CC APPLICANT: the Navy
 CC APPLICANT: U. S. Government, Secretary of
 CC APPLICANT: the Army
 CC TITLE OF INVENTION: Novel Antibodies for Confering Passive
 CC TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
 CC NUMBER OF SEQUENCES: 61
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Howson and Howson

CC STREET: Box 457, 321 Norristown Road
 CC CITY: Spring House
 CC STATE: PA
 CC COUNTRY: USA
 CC ZIP: 19477
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/08435
 CC FILING DATE:
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/941,654
 CC FILING DATE: 09-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Bak, Mary E.
 CC REGISTRATION NUMBER: 31,215
 CC REFERENCE/DOCKET NUMBER: SBC P50107
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (215) 540-9200
 CC TELEFAX: (215) 540-5818
 CC INFORMATION FOR SEQ ID NO. 14:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 122 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 122 AA: 13329 MW: 88138 CN:

Query Match 72.6%; Score 672; DB 11; Length 122;

Best Local Similarity 74.2%; Pred. No. 7.29e-44;

Matches 92; Conservative 15; Mismatches 15; Indels 2; Gaps 2;

Db 1 EVQLLEGGGSLVQPGSSRLKLSCAASGFTFSYAMSVWPAAPGKGLWVAELSDGSKYTY 60
 QY 1 EVQLLEGGGVQVQPRSLFLSCAASGFTFSYAGSMHWVPAAPGKGLWVAGWFGSGNQYY 60
 Db 61 PTVTVGRTPTISDNKNTLYLQMSLRAEDTAVVYCASLIYYG-YDG-YAMDYWGQGTLY 118
 QY 61 SDSVAGRETVPSPDNPSTIFLQMSLPPEDTAVVYCATEVLFPGSKGYYLENWQGTLY 120
 Db 119 TVSS 122
 QY 121 TVSS 124

RESULT 9
 ID PCT-US93-08435-12 STANDARD: PPT: 122 AA.
 XX AC xxxxxx
 XX DT 01-JAN-1900
 XX DE
 XX SE Sequence 12, Application PC/TUS9308435.
 CC Sequence 12, Application PC/TUS9308435
 CC GENERAL INFORMATION:
 CC APPLICANT: SmithKline Beecham, Corporation
 CC APPLICANT: U. S. Government, Secretary of
 CC APPLICANT: the Navy
 CC APPLICANT: U. S. Government, Secretary of
 CC APPLICANT: the Army
 CC TITLE OF INVENTION: Novel Antibodies for Confering Passive
 CC TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
 CC NUMBER OF SEQUENCES: 61
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Howson and Howson
 CC STREET: Box 457, 321 Norristown Road
 CC CITY: Spring House
 CC STATE: PA

CC COUNTRY: USA
CC ZIP: 19477
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: PC-DOS/MS-DOS
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/08435
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/941,654
CC FILING DATE: 09-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Bak, Mary E.
CC REGISTRATION NUMBER: 31,215
CC REFERENCE/DOCKET NUMBER: SBC P50107
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (215) 540-9200
CC TELEFAX: (215) 540-5818
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 122 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 122 AA, 13370 MW, 87746 CN.

Query Match 72.4%; Score 670; DB 11, Length 122;
Best Local Similarity 74.2%; Pred. No. 1,05e-43;
Matches 92; Conservative 14; Mismatches 16, Indels 2; Gaps 2;

Db 1 EVOLLEGGGLVOPGSLRLSCAASGFTFSYAMSWVROAPCKGLEWVSEISDGGSYTY 60
QY 1 EVOLLEGGGLVOPGSLRLSCAASGFTFSYAMSWVROAPCKGLEWVSEISDGGSYTY 60
Db 61 PDVTGRTISRDNSKNTLYLQMNLSLRPDTAVYYCATFVIFGSIKGRYYLENWQGTIV 118
QY 61 SDSVKGRFTVSRDNSRNTLYLQMNLSLRPDTAVYYCATFVIFGSIKGRYYLENWQGTIV 120
Db 119 TVSS 122
QY 121 TVSS 124

RESULT 10
ID US-07-942-245-33 STANDARD; PRT: 125 AA.
AC xxxxxx
XX 01-JAN-1900
DT
DE Sequence 33, Application US/07942245.
XX Sequence 33, Application US/07942245.
CC Patent No. 5639641
CC GENERAL INFORMATION:
CC APPLICANT: PEDERSEN, Jan T.
CC APPLICANT: SEARLE, Stephen M.J.
CC APPLICANT: REES, Anthony R.
CC APPLICANT: ROGUSKA, Michael A.
CC APPLICANT: GOULD, Braydon C.
CC TITLE OF INVENTION: SURFACE PEPTIDE VENERFING OF POTENT
CC NUMBER OF SEQUENCES: 52
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Suchrue, Mion, Zinn, Macpeak & Seas
CC STREET: 2100 Pennsylvania Avenue, N.W.
CC CITY: Washington
CC STATE: D.C.
CC COUNTRY: United States
CC ZIP: 20037-3202

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: HP 9000/700 Workstation
CC SOFTWARE: UNIX
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/942,245
CC FILING DATE: 09-SEP-1992
CC CLASSIFICATION: 530
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (202) 293-7060
CC TELEFAX: (202) 293-7860
CC TELETYPE: 6491103
CC INFORMATION FOR SEQ ID NO: 33:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 125 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 125 AA, 13631 MW, 85784 CN.

Query Match 71.3%; Score 660; DB 7; Length 125;
Best Local Similarity 69.6%; Pred. No. 6.59e-43;
Matches 87; Conservative 19; Mismatches 17, Indels 2; Gaps 2;

Db 1 EVOLVSGGGVOPGSLRLSCSSGFIFFSYAMVWVROAPCKGLEWVA1IWDGSDQHY 60
QY 1 EVOLVSGGGVOPGSLRLSCSSGFIFFSYAMVWVROAPCKGLEWVA1IWDGSDQHY 60
Db 61 ADSVKGRFTISPDNSKNTLYLQMNLSLRPDTAVYYCATFVIFGSIKGRYYLENWQGT 120
QY 61 SDSVKGRFTVSRDNSRNTLYLQMNLSLRPDTAVYYCATFVIFGSIKGRYYLENWQGT 118
Db 121 PVTVS 125
QY 119 LVTVS 123

RESULT 11
ID US-08-305-683A-2 STANDARD; PRT: 142 AA.
AC xxxxxx
XX 01-JAN-1900
DT
DE Sequence 2, Application US/08305683A.
XX Sequence 2, Application US/08305683A.
CC Patent No. 5646041
CC GENERAL INFORMATION:
CC APPLICANT: HARFELDT, Elisabeth
CC APPLICANT: LAKE, Philip
CC APPLICANT: NOTTAGE, Barbara
CC APPLICANT: OSTREPG, Lars G.
CC TITLE OF INVENTION: MONOCLONAL ANTIBODY TO HERPES SIMPLEX
CC NUMBER OF SEQUENCES: 4
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: 379 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: PC-DOS/MS-DOS
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/405,683A
CC FILING DATE: 13-SEP-1994
CC CLASSIFICATION: 424

CC APPLICATION NUMBER: US 07/856,281
 CC FILING DATE: 23-MAR-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/735,064
 CC FILING DATE: 25-JUL-1991
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Teskin Esq., Robin L.
 CC REGISTRATION NUMBER: 35,030
 CC REFERENCE/DOCKET NUMBER: 012712-160
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 703-836-6620
 CC TELEFAX: 703-836-2021
 CC INFORMATION FOR SEQ ID NO: 94:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 123 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: not relevant
 CC TOPOLOGY: not relevant
 CC MOLECULE TYPE: peptide
 CC POSITION IN GENOME:
 CC CHROMOSOME/SEGMENT: RF TS2
 CC SEQUENCE 123 AA: 13515 MW: 82958 CN.
 SQ
 Query Match 71.0%; Score 657; DB 7; Length 123;
 Best Local Similarity 72.4%; Pred. No. 1,14e-42;
 Matches 89; Conservative 19; Mismatches 13; Indels 2; Gaps 2;
 Db 1 QVQLVESGGGVVQPGKSLPLSQAASGFTSSYGMHWVQAPQKGLWVAVSYDGSNEYF 60
 QY
 Db 61 ADSVKGRFTISRDNKNTLYLQMSLRPAEDTAVYVCARDRVAVYASVFFIDSFDIWGQGT 120
 QY
 Db 121 GVT 123
 QY
 Db 119 LVT 121
 RESULT 14
 ID US-08-211-202-141 STANDARD: PRT: 116 AA.
 XX
 AC xxxxxx
 XX
 DT 01-JAN-1900
 XX
 DE Sequence 141, Application US/08211202.
 XX
 CC Sequence 141, Application US/08211202
 CC Patent No. 5565332
 CC GENERAL INFORMATION:
 CC APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
 CC APPLICANT: BAIER, Michael
 CC APPLICANT: JESPER, Laurent Stephane Anne Therese
 CC APPLICANT: WINTER, Gregory Paul
 CC TITLE OF INVENTION: Production of chimeric antibodies - a
 CC TITLE OF INVENTION: combinatorial approach
 CC NUMBER OF SEQUENCES: 144
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
 CC ADDRESS: Borun
 CC STREET: 6300 Sears Tower, 233 South Wacker Drive
 CC CITY: Chicago
 CC STATE: Illinois
 CC COUNTRY: USA
 CC ZIP: 60606-6402
 CC COMPUTER READABLE FORM:
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent in Release #1.0, Version #1.25 (EPC)
 CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/211,202
 CC FILING DATE: 23-SEP-1992
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: GB 9120152.3
 CC FILING DATE: 23-SEP-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: GB 9120377.8
 CC FILING DATE: 25-SEP-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: GB 9206318.9
 CC FILING DATE: 24-MAR-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: GB 9206372.6
 CC FILING DATE: 24-MAR-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/5B92/00883
 CC FILING DATE: 15-MAY-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: David W. Clough
 CC REGISTRATION NUMBER: 36,107
 CC REFERENCE/DOCKET NUMBER: 28111/31960
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 312-474-6300
 CC TELEFAX: 312-474-0448
 CC TELEX: 35-3856
 CC INFORMATION FOR SEQ ID NO: 141:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 116 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 116 AA: 12678 MW: 72426 CN.
 SQ
 Query Match 70.7%; Score 655; DB 6; Length 116;
 Best Local Similarity 76.1%; Pred. No. 1.65e-42;
 Matches 89; Conservative 15; Mismatches 12; Indels 1; Gaps 1;
 Db 1 QVQLVESGGGVVQPGKSLPLSQAASGFTSSYGMHWVQAPQKGLWVAVSYDGSNEYF 60
 QY
 Db 61 ADSVKGRFTISRDNKNTLYLQMSLRPAEDTAVYVCARDRVAVYASVFFIDSFDIWGQGT 116
 QY
 RESULT 15
 ID PCT-US93-10555-6 STANDARD: PRT: 125 AA.
 XX
 AC xxxxxx
 XX
 DT 01-JAN-1900
 XX
 DE Sequence 6, Application PC/TUS9310555.
 XX
 CC Sequence 6, Application PC/TUS9310555
 CC GENERAL INFORMATION:
 CC APPLICANT: SILVERMAN, GREGG J.
 CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
 CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
 CC THROUGH
 CC TITLE OF INVENTION: VACCINATION WITH A R-CELL SUPERNATANT AND CONJUG
 CC ATES
 CC TITLE OF INVENTION: THEREOF
 CC NUMBER OF SEQUENCES: 51
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Jubas & Lubitz
 CC STREET: 1890 Century Park East - Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/10555
CC FILING DATE: 29-OCT-1993
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Howells, Stacy L.
CC REGISTRATION NUMBER: 34,842
CC REFERENCE/COCKET NUMBER: FD-2630
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 125 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: RIV
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..125
CC SEQUENCE 125 AA: 13612 MW: 90692 CN:

Query Match 70.6%; Score 654; DB 11; Length 125;
Best Local Similarity 72.0%; Pred. No. 1.98e-42;
Matches 90; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

Db 1 EVOLVESGGGVVQPGSSSLPLSCAASGFTSSFAMHWVQAPGKGLEWVAVMSYSGENKYY 60
QY 1 EVOLLESGGGVVQPGRSPLSLCAASGFTFSAYGMHWVQAPGKGLEWVAGIWFDSNQYY 60

Db 61 VDSVKGRFTISPNKNTLYLQWNSLPRAEDIALYCAKLSAASGFIFETYGMEWQGITL 120
QY 61 SDSVKGRFTVSRNSPNTLFLQWNSLPPEPTAVYYCAT-EVLFSGIKSPYYLENWGQGITL 119

Db 121 VTVSS 125
QY 120 VTVSS 124

Search completed: Tue Feb 24 07:39:21 1998
Job time : 5 secs.



WIRE

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:12:31 1998; Maspar time 7.36 Seconds
234.122 Million cell updates/sec

Tabular output not generated

Title: >US-08-844-215-5
Description: (1-124) from US08844.15.pep
Perfect Score: 926

Sequence: 1 EVQLLESGGSGVWPGRSLRL IKGPYLENKGGLIVSS 124

Scoring table: PAM 150
Gap 11

Searched: 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq30
1 part1 2 part2 3 part4 4 part5 5 part6 7 part7
8 part8 9 part10 11 part11 12 part12 13 part13
14 part14 15 part15 16 part16 17 part17 18 part18
19 part19 20 part20 21 part21 22 part22 23 part23

Statistics: Mean 30.371; Variance 159.298; scale 0 191

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DR	ID	Description	Pred. No.
1	705	76.2	192	7	R38161	Sequence of the heavy	7 59e-46
2	695	75.1	119	18	R95216	Human foetal immunogl	5 74e-45
3	692	74.7	123	23	W15534	Anti-TGF beta-1 scFv	9 96e-45
4	691	74.6	123	23	W15531	Anti-melanoma antibod	1 26e-44
5	690	74.5	111	2	R12271	Anti-human RhD HAM-R	1 44e-44
6	685	74.0	115	4	R22571	Heavy chain VH3.5 fro	3 60e-44
7	684	73.9	120	17	R52064	Heavy chain variable	4 33e-44
8	683	73.8	123	23	W15535	Anti-TGF beta-1 scFv	5 20e-44
9	683	73.8	141	19	W01522	Monoclonal antibody P	5 20e-44
10	683	73.8	141	23	W24984	Monoclonal antibody P	5 20e-44
11	681	73.5	506	2	R12134	GpF 3 of 4B9 human MA	7 51e-44
12	677	73.1	143	9	R54047	Sequence of the VH re	1 57e-43
13	674	72.8	132	9	R50315	Humanised heavy chain	2 75e-43
14	673	72.7	125	9	P54784	SpA-reactive IgM heav	3 26e-43
15	672	72.6	122	9	R50312	Humanised heavy chain	3 92e-43
16	671	72.5	115	23	W15522	Anti-TGF beta-2 scFv	4 71e-43
17	670	72.4	122	9	R50311	Humanised heavy chain	5 66e-43
18	669	72.2	126	5	R28746	Heavy chain variable	6 80e-43
19	668	72.1	140	23	W15524	Anti-melanoma antibod	8 17e-43
20	664	71.7	117	12	R66323	Human immunoglobulin	1 70e-42

21	664	71.7	123	23	W15536	Anti-TGF beta-1 scFv	1 70e-42
22	664	71.7	126	7	P06519	KOL heavy chain	1 70e-42
23	662	71.5	112	2	R12274	Anti-human RhD REG-A	2 46e-42
24	662	71.5	141	13	P75393	Anti-interleukin-1-31	2 46e-42
25	660	71.3	142	23	W22551	64-963 antibody HSV86	3 55e-42
26	660	71.3	221	10	P56234	162-109/110-61/h-126	3 55e-42
27	656	70.9	459	8	R42066	Human anti-RS heavy	7 39e-42
28	654	70.6	125	9	P54789	SpA-reactive IgM heavy	1 07e-41
29	654	70.6	125	9	P54789	SpA-reactive IgM heavy	1 07e-41
30	653	70.5	124	23	W15537	Anti-melanoma antibod	1 28e-41
31	652	70.4	117	12	R66321	Human immunoglobulin	1 54e-41
32	652	70.4	119	20	W19225	Heavy chain #3 for an	1 54e-41
33	648	70.0	123	23	W09592	Human antibody C4.1 h	3 20e-41
34	648	70.0	140	14	P89480	Anti-human IL-4 human	3 20e-41
35	648	70.0	147	14	P80617	Anti-human IL-4 human	3 20e-41
36	644	69.5	117	23	W15523	Anti-TGF beta-2 scFv	6 57e-41
37	642	69.2	142	5	P31534	MH4H7 MA5 heavy chain	9 52e-41
38	641	69.2	132	6	P30773	Consensus humanised m	1 16e-40
39	641	69.2	140	19	W06205	Xenograft antibody HA	1 16e-40
40	640	69.1	156	6	P24285	Human TNF binding ant	1 39e-40
41	640	69.1	117	17	R52065	Heavy chain variable	1 39e-40
42	640	69.1	118	20	W13921	Heavy chain #1 for an	1 39e-40
43	639	69.0	123	12	R69084	Anti-HIV Fab rev9(VH3	1 57e-40
44	639	69.0	123	22	W08733	Human anti-HIV Fab am	1 57e-40
45	639	69.0	124	23	W15533	Anti-melanoma antibod	1 57e-40

ALIGNMENTS

RESULT 1
ID R38161 standard; Protein: 192 AA.
AC P38161;
DI 01-OCT-1993 (first entry)
DE Sequence of the heavy chain variable region (VH) of human
immunoglobulin G3 (IgG3) produced by transformed human B-cell line
DE 88BV59, ATCC CRL 10624.
KW B-cell; immunoglobulin g; cancer; tumour.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1...113
FT /label= VAR
FT /note= "1st AA is denoted AA#1"
FT Region 31...49
FT /label= CDR 1 50...94
FT Region CDR 2
FT Region CDR 3 95...111
FT /label= CDR 3
FT Region CH 1 112...223
FT /label= CH 1 224...238
FT /label= Hinge 239...242
FT /label= Fab'
FT EP-S46634-A.
PD 16-JUN-1993.
PE 22-OCT-1992, 203827.
PF 13-OCT-1991; US-807300.
PA (ALKU) AK20 NV.
PI Crichton VZ, Haspel MV, Kobrin BJ.
DR WP1; 93-193019/24.
DR N-F52B, Q43772.
DE Transformed human B-cell line for monoclonal antibody produ. for
PT cancer diagnosis - prepd from peripheral blood B-cells of cancer
PT patients actively immunised with autologous tumour antigen, for
PT treating cancers
PS Claim 5; Fig 2, 18pp; English.
CC Q43772 encodes the complete heavy chain from the leader through AAs
CC 212. 88BV59 uses VH31 and a D region which may have resulted from
CC intra D-D recombination and/or gene conversion along with somatic
CC mutation. It is radically different from any germ line D region. It
CC utilises germ line JH3. It is of note that a cysteine at AA posn. 59
CC (AA No. 78 in R38161) is present within the 88BV59 VH. No other

CC human variable region heavy chains have a cysteine at this posn. i.e.
 CC Kabat posn. 59.
 SQ Sequence 192 AA:

Query Match 76.2%; Score 706; DB 7; Length 192;
 Best Local Similarity 77.0%; Pred. No. 7.59e-46;
 Matches 97; Conservative 14; Mismatches 3; Gaps 3;
 Db 20 qvqlvesggvqgprslrlscaasgftfssygmhwrqapkgldwvavisdgscyy 79
 QY 1 EVQLLESGGGVQGPGRSLRLSCAASGFTFSAYGMHWRQAPKGLWVAGIWFVDSNQYY 60
 Db 80 adsvkgrftisrnsntlflqmslraedtavvycvkeg-fgsvvvtthlafdwggqt 138
 QY 61 SDSVKGRFTVSRNSRNTFLQMSLRPEDTAVYICATEVFLFGSIKGRYYLE-N-WGQGT 118
 Db 139 mvtvss 144
 QY 119 LTVSS 124

RESULT 2
 ID R95216 standard; protein; 119 AA.
 AC R95216; (first entry)
 DT 16-DEC-1996
 DE Human foetal immunoglobulin 5opl'CL variable heavy chain.
 KW Antibody; fusion protein; single chain; inhibition; tumour;
 KW diagnosis; detection; imaging; immunotoxin; targeting; assay;
 KW immunoassay; Lewis(Y) carbohydrate antigen.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 31..35
 FT /label= CDR 1.
 FT Domain 50..66
 FT /label= CDR 2.
 FT Domain 99..108
 FT /label= CDR 3.
 FT WO9613594-A1.
 PN 09-MAY-1996.
 PD 26-OCT-1995; U13811.
 PF 28-OCT-1994; US-331398.
 PR 28-OCT-1994; US-331396.
 PR 28-OCT-1994; US-331397.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Benhar I, Brinkmann U, Fitzgerald D, Jung S, Lee B;
 PI Padlan EA, Pai L, Pastan I, Willingham M;
 DR WPI: 96-251462/25.
 PT Single chain fusion proteins and antibodies - useful to diagnose and
 PT treat cancer, specifically bind Lewis(Y) related carbohydrate
 PT antigen

PS Example 13; Figure 11A; 116pp; English.
 CC A novel recombinant DNA molecule which encodes a single chain fusion
 CC protein or antibody comprising the Fv region of both the light and
 CC heavy chains of an antibody (Ab) fused together, and an effector
 CC molecule, where the fusion protein or Ab has the binding specificity
 CC of monoclonal Ab (MAB) B1, B3 or B5, can be used for the production
 CC of such fusion proteins or antibodies. The fusion proteins can be
 CC used in compositions as an immunotoxin to inhibit tumour cell growth.
 CC The single chain antibody can be used to detect the presence or
 CC absence of cells bearing a Lewis(X) carbohydrate antigen in a
 CC patient. The antibodies are also useful as multiple targeting
 CC moieties, providing at least 2 kinds of biological activity. They
 CC can also be used in diagnostic assays and for the imaging of tumours
 CC when attached to a radiolabel and for the pathological diagnosis of
 CC tumours. Humanised antibodies are less immunogenic than the mouse
 CC Mabs B1, B3 and B5, making them more suitable for long term
 CC treatment.
 SQ Sequence 119 AA;

Query Match 75.1%; Score 695; DB 18; Length 119;
 Best Local Similarity 78.2%; Pred. No. 5.74e-45;
 Matches 97; Conservative 14; Mismatches 8; Indels 5; Gaps 2;
 Db 61 adsvkgrftisrnsntlflqmslraedtavvycvkeg-fgsvvvtthlafdwggqt 119

Db 1 qvqlvesggvqgprslrlscaasgftfssygmhwrqapkgldwvavisdgscyy 60
 QY 1 EVQLLESGGGVQGPGRSLRLSCAASGFTFSAYGMHWRQAPKGLWVAGIWFVDSNQYY 60
 Db 61 adsvkgrftisrnsntlflqmslraedtavvycvkeg-fgsvvvtthlafdwggqt 115
 QY 61 SDSVKGRFTVSRNSRNTFLQMSLRPEDTAVYICATEVFLFGSIKGRYYLE-N-WGQGT 120
 Db 116 tvss 119
 QY 121 TVSS 124

RESULT 3
 ID W15534 standard; Protein; 123 AA.
 AC W15534;
 DT 27-NOV-1997 (first entry)
 DE Anti-TGF beta-1 scFv antibody 1-B2 VH domain.
 KW Transforming growth factor beta-1; TGF-beta-1; human;
 KW antibody engineering; scFv; phage display; lung fibrosis;
 KW arterial injury; proliferative retinopathy; retinal detachment;
 KW adult respiratory distress syndrome; liver cirrhosis;
 KW post myocardial infarction; post-angioplasty restenosis;
 KW scleroderma; vascular disease; cataract; glaucoma; scarring;
 KW glomerulonephritis; osteoporosis; immune disease; inflammation;
 KW rheumatoid arthritis; macrophage deficiency disease;
 KW macrophage pathogen infection; therapy.
 OS Homo sapiens.
 FH GB2305921-A.
 FN 23-APR-1997.
 PD 07-OCT-1996; 020920.
 PR 19-JAN-1996; GB-001081.
 PR 06-OCT-1995; GB-020486.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
 PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
 PI Wilton AJ;
 DR WPI: 97-215360/20.
 DR N-PSDB; T60380.
 PT Agent contg. antigen-binding domain of human antibody to
 PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
 PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
 PT immune and inflammatory disease
 PS Claim 16; Fig 1a(1); 184pp; English.
 CC This polypeptide sequence comprises the VH domain of human scFv
 CC antibody 1B2 (also known as 7A3), which is specific for
 CC transforming growth factor (TGF) beta-1. It is encoded by a gene
 CC (T60380) isolated from a peripheral blood lymphocyte library. The
 CC antigen-binding domains of human antibodies (see W15522-40) to TGF
 CC beta-1 and/or beta-2 can be used to counter the adverse effects of
 CC TGF beta, such as (i) promotion of fibrosis (in dermal, ocular or
 CC keloid scarring, lung fibrosis, arterial injury, proliferative
 CC retinopathy, retinal detachment, adult respiratory distress syndrome,
 CC liver cirrhosis, post myocardial infarction, post-angioplasty
 CC restenosis, scleroderma, vascular disorders, cataract, glaucoma, or
 CC esp. neural scarring and glomerulonephritis, also (not claimed)
 CC osteoporosis), or (ii) immune and inflammatory diseases (rheumatoid
 CC arthritis, macrophage deficiency diseases or macrophage pathogen
 CC infection). Nucleic acids encoding human antibody VH and VI can be
 CC used for produ. of recombinant antigen-binding domains. These are
 CC highly specific, have low dissociation constants (pred. less than 5
 CC nM) and low IC50s for neutralisation.
 SQ Sequence 123 AA;

Query Match 74.7%; Score 692; DB 23; Length 123;
 Best Local Similarity 75.8%; Pred. No. 9.96e-45;
 Matches 94; Conservative 15; Mismatches 14; Indels 1; Gaps 1;
 Db 1 qvqlvesggvqgprslrlscaasgftfssygmhwrqapkgldwvavisdgscyy 60
 QY 1 EVQLLESGGGVQGPGRSLRLSCAASGFTFSAYGMHWRQAPKGLWVAGIWFVDSNQYY 60
 Db 61 adsvkgrftisrnsntlflqmslraedtavvycvkeg-fgsvvvtthlafdwggqt 119

QY - 61 SDSVKGPFVTSNSNTLFLQMSLPRDIAVYCAIEVIFGSGKGYVLENWQGTLLV 120
 Db 120 vtss 123
 QY 121 TVSS 124

RESULT 4
 ID W1331 standard; protein: 123 AA.
 AC W1331:
 DT 28-OCT-1997 (first entry)
 DE Anti-melanoma antibody heavy chain clone V575.
 KW Human: monoclonal antitumor antibody; peripheral blood lymphocyte.
 KW cancer: tumorigenesis; anticancer vaccine.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 31..35
 FT /label= CDR1
 FT Region 50..66
 FT /label= CDR2
 FT Region 100..113
 FT /label= CDR3
 PN WC9702479-A2
 PD 23-JAN-1997.
 PF 28-JUN-1996: IB1032.
 PR 30-JUN-1995: US-497647.
 PA (UYVA) UNIV YALE.
 PI Cai X, Garen A;
 DR WPI: 97-109061/10.
 CC Antisense for isolating and synthesizing human monoclonal anti-tumor
 CC antibodies has been produced. The process involves: (a) constructing at
 CC least one fusion gene library from the peripheral blood lymphocytes
 CC (PBLs) of a cancer patient; (b) screening for anti-tumor antibodies in
 CC the phase library in a binding assay with cultured tumor cells of the
 CC same type as the patient's tumor; (c) removing extraneous antibodies by
 CC absorption against normal human cells; (d) cloning the phase selected in
 CC step (b) and (c); (e) assaying the specificity of the cloned phase by
 CC incubating the phase with at least two types of cultured normal cells;
 CC and (f) further testing the specificity of cloned phase that do not bind
 CC to either cell line of cultured normal cells in further binding assays
 CC to cultured tumor cells derived from more than one other tumor that is
 CC not the patient's tumor. The present sequence represents a human heavy
 CC chain antibody, from an scFv antibody fusion phase library, produced by
 CC a method as described above. The antibodies produced can be used for
 CC diagnostic and therapeutic applications and for isolating tumor
 CC antigens for studying tumorigenesis or for use as anti-cancer vaccines.
 CC The human antibodies have low immunogenicity in humans compared to
 CC murine monoclonal antibodies (MAbs). Since the antibodies are isolated
 CC from fusion phase libraries, their affinity and specificity for a
 CC tumor cell line can be improved by genetic manipulations.
 SQ Sequence 123 AA;

Query Match 74.6% Score 631. DB 23. Length 123.
 Best Local Similarity 75.0% Pred No 1.20e-44;
 Matches 93; Conservative 17; Mismatches 12; Indels 2; Gaps 2;
 Db 1 qqlvesggvqprslrlscasagftfssygmhwvrgqpkglwvavlysgdsnkyy 60
 QY 1 EVOLLESGGGVQPGPSRLSLCAASGFTFSAYGMHWVFPQAPGKLEWVAGIWFDPGSGNOY 60
 Db 61 adsvkgrftisrdnsrntlfqlomslrpedtavyycatevlfsgikgyvlenwqgtll 119
 QY 61 SDSVKGPFVTSNSR-NTLFLQMSLPRDIAVYCAIEVIFGSGKGYVLENWQGTLL 119
 Db 120 vtvs 123
 QY 120 VTVS 123

RESULT 5
 ID R12275 standard; Protein: 111 AA.
 AC R12275:
 DT 15-AUG-1991 (first entry)
 DE Anti-human PhD HAM-R MAB (VH chain)
 KW Monoclonal antibody; rhesus D; blood-typing; CDR;
 KW haemolytic disease of the newborn; HDN.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 23..27
 FT /label= CDR1
 FT Region 42..58
 FT /label= CDR2
 FT Region 91 106
 FT /label= CDR3
 PN W09107492-A.
 PD 30-MAY-1991.
 PF 13-NOV-1990: E01964.
 PP 13-NOV-1989: GR-02559n
 PA (BLOO-) CENT BLOOD LAB AUTH.
 PI Hughes- Jones N;
 DR WPI: 91-178104/24.
 DR N-PSDB: Q11957
 CC DNA encoding complementary determining regions - of human
 CC anti-rhesus D antibodies, useful in prodn. of monoclonal
 CC antibodies and for passive immunisation
 CC Disclousure, Fig 14, 32pp, English.
 CC The DNA sequence of eleven monoclonal antibodies are
 CC represented in Q119145-57. Synthetic genes, for both heavy and
 CC light chains may be created by combining selected CDR 1, 2, and 3
 CC regions, which may be selected from different antibody mols. having
 CC varied binding specificity. The chimaeric anti-RbD antibodies can be
 CC used for diagnosis and therapy and are capable of providing blood-
 CC typing reagents of high specificity and reliability. They can also
 CC be used in passive immunisation to prevent haemolytic disease of the
 CC newborn
 SQ Sequence 111 AA;

Query Match 74.5% Score 590; DB 2; Length 111;
 Best Local Similarity 79.5% Pred No 1.44e-44;
 Matches 89; Conservative 13; Mismatches 7; Indels 3; Gaps 3;
 Db 1 ggvvqprslrlscasagftfssygmhwvrgqpkglwvavlysgdsnkyyadvskrf 60
 QY 9 GGVVQPRSLRLSLCAASGFTFSAYGMHWVFPQAPGKLEWVAGIWFDPGSGNOYSDSVKGRF 68
 Db 61 tirdskntlylqmslraedtaavyycatevlfsgikgyvlenwqgtll 111
 QY 69 TVSPKNSNTLFLQMSLPRDIAVYCAIEV-LFGSIKGYV-LENWQGTLL 118

RESULT 6
 ID R22571 standard; Protein: 115 AA.
 AC R22571:
 DT 21-MAY-1992 (first entry)
 DE Heavy chain VH3.5 from BSA binding scFv fragment.
 KW Fd, bacteriophage, gene III, filamentous, phagemid, capsid, coat,
 KW Pils, g3p, binding, adsorption, gene VII, diverse repertoire,
 KW specific binding pairs, replicable genetic display package, human.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 23..27
 FT /label= CDR1
 FT Region 42..58
 FT /label= CDR2
 FT Region 91 106
 FT /label= CDR3
 PN W09107492-A.
 PD 30-MAY-1991.
 PF 10-JUL-1990: G01134.
 PP 10-OCT-1990: GR-015198.
 PP 19-OCT-1990: GR-023845.
 PP 12-NOV-1990: GR-024593.
 PP 06-MAR-1991: GR-004744.
 PP 15-MAY-1991: GR-010549.
 PA (CAMP-) CAMPRIPE ANTIBODY.
 PA (MEDI-) MED RES COUNCIL.
 PI McCafferty J, Pope AP, Johnson KS, Hoogenboom HPJ, Griffiths AD;
 PI Jackson PH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;

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PI Winter GP, Bonnett TP;
 DR WPI: 92-056862/07.
 PT Producing members of specific binding pairs - by expression in
 PT recombinant host cells with a secreting replicable genetic
 PT display package.
 PS Table 11, Page 152; 109pp; English.
 CC PCR was used to prepare a human scFv library from RNA from white
 CC blood cells from an unimmunised donor. Heavy chains from IgG and
 CC IgM antibodies were amplified separately. Four separate libraries
 CC were generated (IgG-K, IgG-lambda, IgM-K and IgM-lambda). The
 CC purified scFv fragments were ligated into the phagemid pHEM1 for
 CC expression on the surface of fd bacteriophage as gene III fusions.
 CC The clones were then subjected to affinity selection for binding
 CC to pHOX:BSA by selection on tubes followed by analysis by ELISA. Of
 CC 96 clones analysed, 43 showed binding to both pHOX:BSA and BSA.
 CC These were designated BSA binders. Thirteen of fourteen clones
 CC sequenced had the same sequence, the VH derived from a human VH3
 CC family gene (shown here) and the VL from a human V lambda 3 family
 CC gene (R22572). The other was derived from a human VH4 family gene
 CC and a human VK1 family gene. One clone bound only to pHOX:BSA
 CC (oxazolone binder). This sequence revealed a VH derived from a
 CC human VH1 family gene (P22569) and VL from a human V lambda 1
 CC family gene (R22570).
 CC See also R21260-307, 309-312, P22450, P22565, P22567-81
 SQ Sequence 115 AA;

Query Match 74.0%; Score 685; DB 4; Length 115;
 Best Local Similarity 78.0%; Pred. No. 3.60e-44;
 Matches 92; Conservative 14; Mismatches 9; Indels 3; Gaps 3;

Db 1 qvqlvsgggvqpqrslrlscaasgftfssygmhvwvrgapkglewavysgdsnkyy 60
 QY 1 EVQLLESGGGVVQPGSRSLRLSCAASGFTFSAYGMHVRQAPKGLIEWVAGIWFDCSNQYY 60

Db 61 adsvkgrftisrdnsntlylqmnsrlraedtavyycaetg-yssgwg-yf-dywdqgt 115
 QY 61 SDSVKGRTVSRRNSRNTLFQMNLSRPEDTAVYYCATEVLFQSGIKGRYILENWQGT 118

RESULT 7
 ID R52064 standard; Protein: 120 AA.
 AC R52064;
 DT 11-OCT-1996 (first entry)
 DE Heavy chain variable region of human G36005 antibody.
 KW antibody; humanised; murine; human; heavy chain; light; variable;
 KW framework region; complementarity determining region; reshaping;
 KW modelling; surface residue; modify.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..30
 FT /label= framework_region_1
 FT /note= "FR 1"
 FT Region 31..35
 FT /label= complementarity_determining_region_1
 FT /note= "CDR 1"
 FT Region 36..49
 FT /note= "FR 2"
 FT Region 50..54
 FT /note= "CDR 2"
 FT Region 55..98
 FT /note= "FR 3"
 FT Region 99..110
 FT /note= "CDR 3"
 FT EP-592106-A1.
 PD 13-APR-1994.
 PF 07-SEP-1993; 307051.
 PR 09-SEP-1992; US-942245.
 PA (PEDE/) PEDERSEN J T.
 PA (IMM-) IMMUNOGEN INC.
 PI Guld BC, Pedersen JT, Rees AP, Roguska MA, Searle SMJ;
 DR WPI: 94-120230/15.
 PT Method of resurfacing of rodent antibodies to produce humanised
 PT antibody forms - for producing non-human antibodies with improved

therapeutic efficiency by presenting human surface on V-region
 Example 1; Fig 4B; 230pp; English.
 CC Modification of a rodent antibody (Ab) or fragment by resurfacing in
 CC order to produce a humanised rodent Ab can be determined by calculating
 CC homology between murine and human Ab antibody surfaces. In order to test
 CC the resurfacing approach of the invention, three humanisation experiments
 CC were set up: (1) traditional loop grafting; (2) resurfacing approach
 CC using most similar chain; and (3) resurfacing approach using human
 CC sequences with similar surface residues. The Ab used was the murine
 CC anti-N901 Ab (see R52064). Experiment 2 was carried out using the present
 CC sequence which represents the human G36005 Ab heavy chain variable region
 CC with 89 percent homology with anti-N901 Ab. N901/G36005 (R52065) was
 CC prepared by CDR grafting. Sequence numbering starts at 118 in the
 CC specification.
 SQ Sequence 120 AA;

Query Match 73.9%; Score 684; DB 17; Length 120;
 Best Local Similarity 77.2%; Pred. No. 4.31e-44;
 Matches 95; Conservative 14; Mismatches 11; Indels 3; Gaps 2;

Db 1 qvqlvsgggvqpqrslrlscaasgftfssygmhvwvrgapkglewavysgdsnkyy 60
 QY 1 EVQLLESGGGVVQPGSRSLRLSCAASGFTFSAYGMHVRQAPKGLIEWVAGIWFDCSNQYY 60

Db 61 adsvkgrftisrdnsntlylqmnsrlraedtavyycaetg-yf-dywdqgt 117
 QY 61 SDSVKGRTVSRRNSRNTLFQMNLSRPEDTAVYYCATEVLFQSGIKGRYILENWQGT 120

Db 118 tvs 120
 QY 121 tvs 123

RESULT 8
 ID W15535 standard; Protein: 123 AA.
 AC W15535;
 DT 27-NOV-1997 (first entry)
 DE Anti-TGF beta-1 scFv antibody 3109 VH domain.
 KW Transforming growth factor beta-1; TGF-beta-1; human;
 KW antibody engineering; scFv; phage display; lung fibrosis;
 KW arterial injury; proliferative retinopathy; retinal detachment;
 KW adult respiratory distress syndrome; liver cirrhosis;
 KW post myocardial infarction; post-angioplasty restenosis;
 KW scleroderma; vascular disease; cataract; glaucoma; scarring;
 KW glomerulonephritis; osteoporosis; immune disease; inflammation;
 KW rheumatoid arthritis; macrophage deficiency disease;
 KW macrophage pathogen infection; therapy.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 1..30
 FT /label= framework_region_1
 FT /note= "FR 1"
 FT Region 31..35
 FT /label= complementarity_determining_region_1
 FT /note= "CDR 1"
 FT Region 36..49
 FT /note= "FR 2"
 FT Region 50..54
 FT /note= "CDR 2"
 FT Region 55..98
 FT /note= "FR 3"
 FT Region 99..110
 FT /note= "CDR 3"
 FT EP-592106-A1.
 PD 13-APR-1994.
 PF 07-SEP-1993; 307051.
 PR 09-SEP-1992; US-942245.
 PA (PEDE/) PEDERSEN J T.
 PA (IMM-) IMMUNOGEN INC.
 PI Guld BC, Pedersen JT, Rees AP, Roguska MA, Searle SMJ;
 DR WPI: 94-120230/15.
 PT Method of resurfacing of rodent antibodies to produce humanised
 PT antibody forms - for producing non-human antibodies with improved

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CC This is the amino acid sequence of the heavy chain variable (Vh) region
 CC from the human monoclonal antibody (MAB) PE1-1. The MAB was generated
 CC by immunising humans with a hepatitis B virus (HBV) vaccine, isolating
 CC peripheral blood lymphocytes (PBL) and fusing them with a mouse/human
 CC xenogeneic cell line SP2-4. 5 cell lines were isolated: PE1-1, ZM1-1,
 CC ZM1-2, MD3-4 and LO3-3. The cell lines were then tested for production
 CC of an anti-hepatitis B virus surface antigen antibody by ELISA. The MABs
 CC are then purified from large scale cell culture by protein A
 CC chromatography, size separation on Sephacryl S300 gel and ion exchange
 CC chromatography on Q-Sepharose. The heavy and light chains of the MABs
 CC were isolated and their amino acid sequences determined. Primers were
 CC generated and used to amplify cDNA synthesised from RNA purified from
 CC each hybridoma cell line. The sequences of the heavy and light chains
 CC (nucleic acid and amino acid) from MABs PE1-1, ZM1-2 and MD3-4 are
 CC shown in T85838-45 and W24984-91. The MABs can be used to treat HBV
 CC infections in immunosuppressed patients or patients with chronic active
 CC hepatitis, especially liver transplant patients.
 CC Sequence 141 AA:

Query Match 73.8%; Score 683; DB 23; Length 141;
 Best Local Similarity 77.6%; Pred. No. 5.20e-44;
 Matches 97; Conservative 10; Mismatches 14; Indels 4; Gaps 2;

DB 20 qvqlvesggvqpgsrslrslscasgftfrsrygmhwrqapqgkglewvavisdgskwy 79
 QY 1 EVQLLESGGGVQPGSRSLRSLSCASGFTFSAYGMHWRQAPQPGKGLWVAVIGWFGDSNOYY 60
 DB 80 adskvgrftisrdnsrntflgmhslraadtgvvyccakdqlyfgsqspqhy---vvgqgtl 136
 QY 61 SDSVKGRFTVSPRNSRNTFLQMSLRPDTAVYYCATEVL-FGSIKGRYYLENWGQJTL 119
 DB 137 vtvs 141
 QY 120 VTVSS 124

RESULT 11
 ID R12134 standard; Protein: 506 AA.
 AC R12134;
 DT 01-AUG-1991 (first entry)
 DE ORF 3 of 4B9 human MAB heavy chain variable region clone.
 KW immunoglobulin G; heavy chain; variable region; duplication.
 KW passive immunity; group B streptococci.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 244...369
 FT /label= L/V region
 FT /note= "last 3 residues of leader and variable
 FT region; the rest of leader is translated in
 FT ORF 1"
 PN WO9106305-A.
 PD 16-MAY-1991.
 PF 06-NOV-1990: U06426.
 PR 07-NOV-1989; US-432700.
 PA (BRIM) BRISTOL-MYERS SQUIB.
 PI Shuford WM, Harris LJ, Rafi HV;
 WPI: 91-163947/22.
 DR N-PSDB: Q11880.
 PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT class
 PS Example 4; Fig 18; 104pp; English.
 CC This sequence is derived from the nucleotide sequence encoding the
 CC heavy chain variable region. The "x" residues represent nonsense
 CC codons. The coding sequence has been translated in all 3 reading
 CC frames (see also R12132 and R12133).
 CC See also Q11878 and Q11879.
 CC Sequence 506 AA:
 Query Match 73.5%; Score 681; DB 2; Length 506;
 Best Local Similarity 76.6%; Pred. No. 7.51e-44;
 Matches 95; Conservative 14; Mismatches 13; Indels 2; Gaps 1;

DB 247 qvqlvesggvqpgsrslrslscasgftfrsrygmhwrqapqgkglewvavisdgskwy 406
 QY 1 EVQLLESGGGVQPGSRSLRSLSCASGFTFSAYGMHWRQAPQPGKGLWVAVIGWFGDSNOYY 60
 DB 307 adskvgrftisrdnsrntflgmhslraadtgvvyccakdqlyfgsqspqhy---vvgqgtl 464
 QY 61 SDSVKGRFTVSPRNSRNTFLQMSLRPDTAVYYCATEVL-FGSIKGRYYLENWGQJTL 120
 DB 365 tvss 368
 QY 121 VTVSS 124

RESULT 12

ID R54047 standard; Protein: 143 AA.
 AC R54047;
 DT 08-NOV-1994 (first entry)
 DE Sequence of the VH region of monoclonal antibody PE1-1 against
 DE hepatitis B virus surface antigen.
 KW Hepatitis B virus; surface antigen; monoclonal antibody; therapy;
 KW HBsAg; diagnosis; HBV.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1...19
 FT /label= leader
 FT Region 20...117
 FT /label= VH III
 FT Region 50...54
 FT /label= CDR 1 69...85
 FT /label= CDR 2 118...129
 FT /label= D 130...143
 FT /label= JH 4
 PN WO9411495-A.
 PD 26-MAY-1994.
 PR 06-NOV-1992: U09749.
 PR 06-NOV-1992: WO-U09749.
 PA (SANO) SANDOZ LTD.
 PI Ostberg LG;
 WPI: 94-183497/22.
 DR N-PSDB: O64050.
 PT Monoclonal antibodies active against Hepatitis B surface antigen
 PT - for diagnosis and treatment of Hepatitis B virus
 PS Example; Page 35; 53pp; English.
 CC Human volunteers were immunised with hepatitis B vaccine. MD3-4, ZM1-
 CC 2, ZM1-1 and PE1-1 hybridoma cell lines were derived from
 CC lymphocytes of individuals immunised with Heptavax (Merck & Co).
 CC Antibodies PE1-1, ZM1-1, ZM1-2 and MD3-4 belong to the IgG1 class.
 CC The cell lines producing PE1-1, ZM1-1 and ZM1-2 were deposited as
 CC ATCC HB9234, 9191 and 9192 respectively. The cell lines all behave
 CC as typical (mouse x human) x human hybridomas and produce their
 CC respective Abs in concs. ranging up to 25 mg/l in standard
 CC suspension culture. The heavy variable (VH) and light variable (LH)
 CC chains of Abs PE1-1, ZM1-1, ZM1-2 and MD3-4 were isolated and
 CC sequenced. Total RNA was extracted from 10(7) hybridoma cells
 CC of each cell line. ss DNA was synthesised using AMV-reverse
 CC transcriptase and oligo-dT as primer. PCR were performed and
 CC amplified DNA was size selected. ss DNA for sequencing was isolated
 CC from each positive clone after superinfection with M13K07.
 CC Sequencing was by the dideoxy chain termination method (Sanger
 CC et al.).
 SQ Sequence 143 AA:

Query Match 73.1%; Score 677; DB 9; Length 143;
 Best Local Similarity 76.6%; Pred. No. 1.57e-43;
 Matches 95; Conservative 11; Mismatches 14; Indels 4; Gaps 2;

DB 20 qvqlvesggvqpgsrslrslscasgftfrsrygmhwrqapqgkglewvavisdgskwy 79
 QY 1 EVQLLESGGGVQPGSRSLRSLSCASGFTFSAYGMHWRQAPQPGKGLWVAVIGWFGDSNOYY 60

TT	TURN	62	67
FT	STRAND	58	73
TT	TURN	74	77
FT	STRAND	78	83
TT	HELI	88	90
FT	STRAND	92	99
TT	STRAND	106	106
FT	TURN	107	108
FT	STRAND	109	109
FT	STRAND	113	113
FT	STRAND	120	124
FT	STRAND	126	126
FT	STRAND	137	137
FT	STRAND	143	143
FT	STRAND	150	150
FT	STRAND	157	157
FT	STRAND	164	164
FT	STRAND	171	171
FT	STRAND	178	178
FT	STRAND	185	185
FT	STRAND	192	192
FT	STRAND	199	199
FT	STRAND	206	206
FT	STRAND	213	213
FT	STRAND	220	220
FT	STRAND	227	227
FT	STRAND	234	234
FT	STRAND	241	241
FT	STRAND	248	248
FT	STRAND	255	255
FT	STRAND	262	262
FT	STRAND	269	269
FT	STRAND	276	276
FT	STRAND	283	283
FT	STRAND	290	290
FT	STRAND	297	297
FT	STRAND	304	304
FT	STRAND	311	311
FT	STRAND	318	318
FT	STRAND	325	325
FT	STRAND	332	332
FT	STRAND	339	339
FT	STRAND	346	346
FT	STRAND	353	353
FT	STRAND	360	360
FT	STRAND	367	367
FT	STRAND	374	374
FT	STRAND	381	381
FT	STRAND	388	388
FT	STRAND	395	395
FT	STRAND	402	402
FT	STRAND	409	409
FT	STRAND	416	416
FT	STRAND	423	423
FT	STRAND	430	430
FT	STRAND	437	437
FT	STRAND	444	444
FT	STRAND	451	451
FT	STRAND	458	458
FT	STRAND	465	465
FT	STRAND	472	472
FT	STRAND	479	479
FT	STRAND	486	486
FT	STRAND	493	493
FT	STRAND	500	500
FT	STRAND	507	507
FT	STRAND	514	514
FT	STRAND	521	521
FT	STRAND	528	528
FT	STRAND	535	535
FT	STRAND	542	542
FT	STRAND	549	549
FT	STRAND	556	556
FT	STRAND	563	563
FT	STRAND	570	570
FT	STRAND	577	577
FT	STRAND	584	584
FT	STRAND	591	591
FT	STRAND	598	598
FT	STRAND	605	605
FT	STRAND	612	612
FT	STRAND	619	619
FT	STRAND	626	626
FT	STRAND	633	633
FT	STRAND	640	640
FT	STRAND	647	647
FT	STRAND	654	654
FT	STRAND	661	661
FT	STRAND	668	668
FT	STRAND	675	675
FT	STRAND	682	682
FT	STRAND	689	689
FT	STRAND	696	696
FT	STRAND	703	703
FT	STRAND	710	710
FT	STRAND	717	717
FT	STRAND	724	724
FT	STRAND	731	731
FT	STRAND	738	738
FT	STRAND	745	745
FT	STRAND	752	752
FT	STRAND	759	759
FT	STRAND	766	766
FT	STRAND	773	773
FT	STRAND	780	780
FT	STRAND	787	787
FT	STRAND	794	794
FT	STRAND	801	801
FT	STRAND	808	808
FT	STRAND	815	815
FT	STRAND	822	822
FT	STRAND	829	829
FT	STRAND	836	836
FT	STRAND	843	843
FT	STRAND	850	850
FT	STRAND	857	857
FT	STRAND	864	864
FT			

DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG HEAVY CHAIN V-III REGION (NIE).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 77070269.
 RA PONTING L., HILSCHMANN N.;
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1573-1604(1976).
 RN [2]
 RP DISULFIDE BOND.
 RX MEDLINE; 77070267.
 RA DREKER L., SCHWARZ J., PEICHEL W., HILSCHMANN N.;
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1515-1540(1976).
 CC -1- THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.
 DR PIR: A02053; GLHUNI.
 DR HSSP: P01607; IFGV.
 KW IMMUNOGLOBULIN V REGION.
 FT MOD.PES 1 1 PYRROLIDONE CARBOXYLIC ACID
 FT DISULFID 22 96
 FT NON-TER 119 119
 SQ SEQUENCE 119 AA: 13242 MW: 5703CA8E CRC32:

Query Match 64.7%; Score 596; DB 5; Length 119;
 Best Local Similarity 64.8%; Pred. No. 1,678-102;
 Matches 81; Conservative 23; Mismatches 15; Indels 6; Gaps 4;
 Db 1 qvqlsgggvqvqgrslrlscasagfftsrtythwvrgagkglewavmsybgbbkhy 60
 QY 1 EVQLLESGGGVVQPGPSLRLSCAASGFFTKYTGMMHWVQAPKGLGWAGISFGSNQYY 60
 Db 61 adsvngrftisrndskntlylmnsrlrpedtavvyari--r-dtam--ff-ahwgggtl 114
 QY 61 ADSVNGRFTIVSPNSPDTVFLQMSLSRLPEDIATVYVCATEGSPFGSIKGRYYLENWGGTL 120
 Db 115 vtvs 119
 QY 121 VTVSS 125

RESULT 6
 ID HV3A HUMAN STANDARD; PRT; 117 AA.
 AC P01764;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PPFCPSOP V-III REGION (VH26)
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 81101090
 RA MATTHEYSENS G., RABBITTS T.H.;
 RL PPOC NATL. ACAD. SCI. U.S.A. 77:6561-6565(1980).
 DR EMBL; J00236; G553412;
 DR EMBL; M35415; G553422;
 DR PIR; A02047; H3H026.
 DR HSSP: P01772; IIGM.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-II REGION (VH26)
 FT NON-TER 117 117
 SQ SEQUENCE 117 AA: 12582 MW: 15A21B2A CRC32:

Query Match 62.8%; Score 578; DB 5; Length 117;
 Best Local Similarity 77.3%; Pred. No. 1,518-98;
 Matches 75; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Db 20 evqllesggglvqpqgrslrlscasagfftsrtythwvrgagkglewavmsybgbbkhy 70

QY 1 EVQLLESGGGVVQPGPSLRLSCAASGFFTKYTGMMHWVQAPKGLGWAGISFGSNQYY 60
 Db 80 gdsykgdfstisrndskntlylmnsrlrpedtavvyari--r-dtam--ff-ahwgggtl 116
 QY 61 ADSVNGRFTIVSPNSPDTVFLQMSLSRLPEDIATVYVCATEGSPFGSIKGRYYLENWGG 97

RESULT 7
 ID HV3A HUMAN STANDARD; PRT; 120 AA.
 AC P01766;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V-III REGION (BRO).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 77117674.
 RA CAPPA J.D., HOPPE J.F.;
 RL IMMUNOCHEMISTRY 13:905-909(1976)
 CC -1- THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE SERUM OF A
 CC PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM TYPE.
 DR PIR: A02049; M3HUBW.
 DR HSSP: P01772; IFGV.
 KW IMMUNOGLOBULIN V REGION.
 FT NON-TER 120 120
 SQ SEQUENCE 120 AA: 13227 MW: B404C4F1 CRC32:

Query Match 62.8%; Score 578; DB 5; Length 120;
 Best Local Similarity 65.9%; Pred. No. 1,518-98;
 Matches 81; Conservative 19; Mismatches 17; Indels 6; Gaps 4;
 Db 1 evqllesggglvqpqgrslrlscasagfftsrtythwvrgagkglewavmsybgbbkhy 59
 QY 1 EVQLLESGGGVVQPGPSLRLSCAASGFFTKYTGMMHWVQAPKGLGWAGISFGSNQYY 60
 Db 60 adsvkgdfstisrndskntlylmnsrlrpedtavvyari--spvslrvgdsklyllygsvrvgg 117
 QY 61 ADSVKGDFIVSPNSPDTVFLQMSLSRLPEDIATVYVCATEGSPFGSIKGRYYLENWGG 117
 Db 118 gtl 120
 QY 118 GTL 120

RESULT 8
 ID HV3A HUMAN STANDARD; PRT; 122 AA.
 AC P01762;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V-III REGION (TRO).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE (MYELOMA PROTEIN TPO).
 RX MEDLINE; 76023781.
 RA KPAZIN H., ALTEVOGT P., PUGHAN F., KOPPT A., STAPOSCIR K.;
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 356:1337-1342(1975).
 CC -1- THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
 DR PIR: A02045; A1HUTP.
 DR HSSP: P01772; 8FAB.
 KW IMMUNOGLOBULIN V REGION.
 FT MOD.PES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON-TER 122 122
 SQ SEQUENCE 122 AA: 13472 MW: BF02D3E8 CRC32:

Query Match 62.9%; Score 579; DB 5; Length 122;

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Best Local Similarity 56.8%; Pred. No. 1,51e-98;
Matches 71; Conservative 29; Mismatches 22; Indels 3; Gaps 2;

Db 1 qvllvsggggllvkgqgslrlscvasgfdrfdymwlrztpgkglzwsvyigsgstlyy 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLESGGGVQPGRSRLSCASGTFKTYGMHWROAPGKGLEWVAGISFDGSGNOY 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 adsvkgrftisrdnaqsklylzmbslrlzbtavvycaatbb-fbw--stslbywqzqbl 117
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ADSVKGRFTVSRNSRDTVFLOMSS:PLEDTAVVYCATGSPFGSIKGRYVLENWQQTGL 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 118 vtvs 122
    :|||||
QY 121 VTSS 125
    :|||||

RESULT 9
ID HV3L HUMAN STANDARD: PRT: 119 AA.
AC P0173:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (BUR).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE (MYELOMA PROTEIN BUR).
RX MEDLINE: 79151016.
RA PUTNAM F.W., LIU Y.-S.V., LOW T.T.K.;
RL J. BIOL. CHEM. 254:2865-2874(1979)
DR PIR: A02056; ALHUBR.
DR HSSP: P01772; 1FGV.
KW IMMUNOGLOBULIN V REGION: GLYCOPROTEIN.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT CARBOHYD 28 28
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 12981 MW; 323A4FE1 CRC32:

Query Match 62.6%; Score 577; DB 5; Length 119;
Best Local Similarity 63.7%; Pred No 2 50e-98;
Matches 79; Conservative 22; Mismatches 17; Indels 6; Gaps 2.

Db 1 qvllvsgggvqgqsklrlscstasafnlsdyamhwrdapqkglzwvallysgstlyy 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLESGGGVQPGRSRLSCASGTFKTYGMHWROAPGKGLEWVAGISFDGSGNOY 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 adsvgrftisrbiskbtlylzmktlrltdtavvycaakliavagt---rbf---wggqtl 114
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ADSVKGRFTVSRNSRDTVFLOMSSRLDTAVVYCATGSPFGSIKGRYVLENWQQTGL 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 115 vtvs 118
    :|||||
QY 121 VTSS 124
    :|||||

RESULT 10
ID HV3L HUMAN STANDARD: PRT: 120 AA.
AC P01782:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (DOR).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 80020921.
RA STEINER L.A., GARCIA PARDO A., MARGOLIES M.N.;
RL BIOCHEMISTRY 18:4068-4080(1979).
RN [2]

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CRYSTALLIZATION.
RP MEDLINE: 80020920.
RA STEINER L.A., LOPES A.D.;
RL BIOCHEMISTRY 18:4054-4067(1979).
CC -1- THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE HINGE REGION.
CC THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN DISULFIDE BONDS.
DR PIR: A02065; GIHUBB.
DR HSSP: P01789; 2FGW.
KW IMMUNOGLOBULIN V REGION.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13440 MW; 100C1E0F CRC32:

Query Match 61.2%; Score 564; DB 5; Length 120;
Best Local Similarity 63.2%; Pred. No. 1,78e-95;
Matches 79; Conservative 21; Mismatches 20; Indels 5; Gaps 4.

Db 1 evqlvesggdlvqparslrlscasafnlnhmlwlrztpgkglzwvallysgstlyy 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLESGGGVQPGRSRLSCASGTFKTYGMHWROAPGKGLEWVAGISFDGSGNOY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 adsvkgrfaisrdnaqsklylqnlrlpedtafyycak-q--yiw-nawwfdswqgatl 115
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ADSVKGRFTVSRNSRDTVFLOMSSRLDTAVVYCATGSPFGSIKGRYVLENWQQTGL 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 116 vtvs 120
    :|||||
QY 121 VTSS 125
    :|||||

RESULT 11
ID HV3L HUMAN STANDARD: PRT: 116 AA.
AC P01781:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (GAL).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 75059123.
RA WATANABE S., RAPIKOL H.U., HORN J., BERTRAM J., HILSCHMANN N.;
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 354:1505-1509(1973).
RN [2]
RP REVISION TO THE COMPOSITION OF 28-33.
RA HILSCHMANN N.;
RL SUBMITTED (JUN-1975) TO THE PIR DATA BANK.
CC -1- THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
DR PIR: A02064; M3HUGL.
DR HSSP: P01607; 1FGV.
KW IMMUNOGLOBULIN V REGION.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12730 MW; F112826C CRC32:

Query Match 60.8%; Score 560; DB 5; Length 116;
Best Local Similarity 67.2%; Pred No. 1,34e-94;
Matches 84; Conservative 16; Mismatches 14; Indels 9; Gaps 4.

Db 1 evqlvesggdlvqparslrlscasafnlnhmlwlrztpgkglzwvallysgstlyy 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLESGGGVQPGRSRLSCASGTFKTYGMHWROAPGKGLEWVAGISFDGSGNOY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 vdsvkgrfaisrdnaqsklylqnlrlpedtafyycak-q--wpp--rdy---wqgatl 111
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ADSVKGRFTVSRNSRDTVFLOMSSRLDTAVVYCATGSPFGSIKGRYVLENWQQTGL 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 112 vtvs 116
    :|||||
QY 121 VTSS 125
    :|||||

RESULT 12

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ID  HV3N_HUMAN          STANDARD:          PRT:  119 AA.
AC  P01775:
DT  21-JUL-1986 (REL. 01, CREATED)
DT  21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT  21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE  IG HEAVY CHAIN V-III REGION (1AY).
OS  HOMO SAPIENS (HUMAN).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC  EUTHERIA; PRIMATES.
RN  [1]
RP  SEQUENCE.
RX  MEDLINE; 75046755.
RA  CAPRA J.D., KEHOE J.M.;
RL  PROC. NATL. ACAD. SCI. U.S.A. 71:4032-4036(1974)
CC  -!- THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN
CC  ACTIVITY.
DR  PIR: A02058; M3HUPJ.
KW  IMMUNOGLOBULIN V REGION.
FT  NON_TER 119
SQ  SEQUENCE 119 AA; 12858 MW; 1CE0116C CRC32;

Query Match      60.5%; Score 557; DB 5; Length 119;
Best Local Similarity 59.0%; Pred. No. 6,08e-94;
Matches 72; Conservative

Db  2 vqllesggglvpggslrlscaasgffissamswvrcapkgkglewva-wkyengndkhy 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  2 vqllesgggvpqgsrlscaasgfftktygmhmvrcapkgkglewvagsfd-GSNQYY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  61 adsvgrfctisrdsnkntlylqmgqlqzvaaiyycardagpy--vsptff-abwgggtl 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  61 ADSVKGFPIVSPNSPDIVFLQMSLRLEDTAIVYVCATEGSPFGSIKGPYVLENWGGTGL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  118 vt 119
    ||
QY  121 vt 122

RESULT  13
ID  HV16_MOUSE          STANDARD:          PRT:  136 AA.
AC  P01783;
DT  21-JUL-1986 (REL. 01, CREATED)
DT  21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT  01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE  IG HEAVY CHAIN PRECURSOR V REGION (MOPC 21) (FRAGMENT).
OS  MUS MUSCULUS (MOUSE).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
OC  EUTHERIA; RODENTIA.
RN  [1]
RP  SEQUENCE FROM N A.
RX  MEDLINE; 81234548.
RA  BOWELL A.L.M., PASKIND M., PETH M., IMANISHI-KAPI T., PAJENSKY K
RA  BALTIMORE D.;
RL  CELL 24-635-637(1991);
RN  [2]
RP  SEQUENCE OF 17-136
RX  MEDLINE; 77100368.
RA  ADEUGBO K., MILSTEIN C., SECHER D.S.;
RL  NATURE 265:299-304(1977).
DR  EMBL; J00522; G195055; -.
DR  PIR: A02066; GIMS21.
DR  HSP: P01607; 1FGV.
KW  IMMUNOGLOBULIN V REGION; SIGNAL.
FT  NON_TER 1
FT  SIGNAL <1 16
FT  CHAIN 17 136
FT  DOMAIN 115 119
FT  DOMAIN 120 136
FT  DISULFID 38 112
FT  NON_TER 136 136
FT  NON_TER 75 78
FT  CONFLICT 89 90
HYAD -> DYAH (IN REF. 2)
EN -> ND (IN REF. 2)

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FT  CONFLICT 115 115      W -> H (IN REF. 2).
FT  CONFLICT 120 120      Y -> K (IN REF. 2).
SQ  SEQUENCE 136 AA; 15071 MW; 24BFDEB8 CRC32;

Query Match      60.3%; Score 555; DB 5; Length 136;
Best Local Similarity 65.6%; Pred. No. 1.67e-93;
Matches 82; Conservative 20; Mismatches 18; Indels 5; Gaps 3;

Db  17 dvqlvesggglvpggslrlscaasgffissgmhwvrcapkgkglewva-ysgsgstlhy 76
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  1 EVOLLESGGGVVQPSRLSLSCAASGFFTKTYGMHWRVQAPKGLEWVAGISFDGSNOYY 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  77 adtkcrftisrdsnkntlylqmtslrsedtamycarwgn-y-py--yyandywqgqts 131
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  61 ADSVKGFPIVSPNSPDIVFLQMSLRLEDTAIVYVCATEGSPFGSIKGPYVLENWGGTGL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  132 vtss 136
    |||||
QY  121 vtss 125

RESULT  14
ID  HV3M_HUMAN          STANDARD:          PRT:  119 AA.
AC  P01774;
DT  21-JUL-1986 (REL. 01, CREATED)
DT  21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT  21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE  IG HEAVY CHAIN V-III REGION (POM)
OS  HOMO SAPIENS (HUMAN).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC  EUTHERIA; PRIMATES.
RN  [1]
RP  SEQUENCE.
RX  MEDLINE; 75046755.
RA  CAPRA J.D., KEHOE J.M.;
RL  PROC. NATL. ACAD. SCI. U.S.A. 71:4032-4036(1974)
CC  -!- THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN
CC  ACTIVITY.
DR  PIR: A02057; M3HUPM.
DR  HSP: P01772; 1FGV.
KW  IMMUNOGLOBULIN V REGION
FT  VARIANT 54 54
FT  NON_TER 119 119
SQ  SEQUENCE 119 AA; 12953 MW; 2A5697D2 CRC32;

Query Match      59.4%; Score 547; DB 5; Length 119;
Best Local Similarity 59.4%; Pred. No. 9.37e-92;
Matches 73; Conservative 28; Mismatches 17; Indels 5; Gaps 4;

Db  1 evqllesggglvpggslrlscaasgffissamswvrcapkgkglewva-wkyengndkh 59
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  1 EVOLLESGGGVVQPSRLSLSCAASGFFTKTYGMHWRVQAPKGLEWVAGISFDGSNOYY 59
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  60 yadsvgrfctisrdsnkntlylqmtslrsedtamycardagpy--vsptff-abwgggt 116
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  60 YADSVKGFPIVSPNSPDIVFLQMSLRLEDTAIVYVCATEGSPFGSIKGPYVLENWGGTGL 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  117 lvt 119
    |||
QY  120 lvt 122

RESULT  15
ID  HV3F_HUMAN          STANDARD:          PRT:  115 AA.
AC  P01767;
DT  21-JUL-1986 (REL. 01, CREATED)
DT  21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT  21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE  IG HEAVY CHAIN V-III REGION (BUT).
OS  HOMO SAPIENS (HUMAN).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC  EUTHERIA; PRIMATES.

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Thu Feb 26 07:06:04 1998

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RN  SEQUENCE.
RP  MEDLINE: 78137069.
RX  TORANO A.; PUTNAM F.W.;
RA  PROC. NATL. ACAD. SCI. U.S.A. 75:966-969(1978).
RL  CC -!- THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C REGION OF THIS
CC  MYELOMA PROTEIN IS ALSO GIVEN.
DR  PIR: A02050; A2HUBU.
DR  HSP: P01772; IFGV.
KW  IMMUNOGLOBULIN V REGION.
FT  NON_TER 115 115
SQ  SEQUENCE 115 AA: 12379 MW: 90803472 CPC32;

Query Match      59.1%; Score 544; DB 5; Length 115;
Best Local Similarity 69.7%; Pred. No. 4.24e-91;
Matches 69, Conservative 17; Mismatches 12; Indels 1; Gaps 1;

Db 1  evqlvetgggllqpqgsrlrscasgftvshhmswvrqapdkalzwxysai-yrgattvy 59
    ||||..||||..||||..||||..||||..||||..||||..||||..||||..||
QY 1  EVQLLESGGGVYVQPGKSLRLSCAASGFTFKTYGMHWVRQAPGKLEWVAGLSFDGSNQYY 60
    ||||..||||..||||..||||..||||..||||..||||..||||..||||..||

Db 60  adsvkrftisrddrbtvyqlmbslraedtavyyvcard 98
    ||||..||||..||||..||||..||||..||||..||||..||||..||||..||
QY 61  ADSVKGRFIVSRDNRDVFVFLQMSSLRLIEDTAVYYCATE 99
    ||||..||||..||||..||||..||||..||||..||||..||||..||||..||

Search completed: Tue Feb 24 07:09:20 1998
Job time : 15 secs.

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Query Match      72.6%; Score 672; DB 9; Length 122;
Best Local Similarity 74.2%; Pred. NO. 3.92e-43;
Matches 92; Conservative 15; Mismatches 15; Indels 2; Gaps 2;

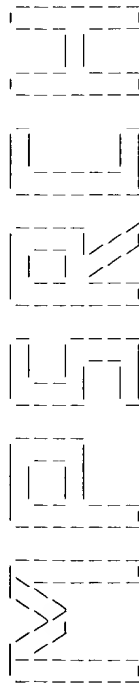
Db 1  exqlllesggglvqpqgsrlrlscaasgftfssyamswwrqapqkglewvseisdqgsytyy 60
QY 1  EVOLLESGGGVVQPGFSLRLSCAASGFTFSAYGMHWRQAPQKGLEWVAGIWFQGSNQYY 60

Db 61  pdtvtgrftisrdnsknltlylqmnslraedtavvyacasliyyg-ydq-yandywdqgtlv 118
QY 61  SDSVKGRFTVSPDNRNTLFIQMNLSLPEDTAVVYVCATEVLFGSIKQPYYLENNMGQGTIV 120

Db 119  tvss 122
QY 121  tvss 124

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Search completed: Tue Feb 24 07:13:04 1998
Job time : 33 secs.



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ORGANISM      #formal_name Homo sapiens #common_name man
DATE          31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
ACCESSIONS    A60943; A48165
REFERENCE     Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.;
#authors      Alt, F.W.; Kabat, E.A.; Latov, N.
#journal      J. Neuroimmunol. (1990) 30:245
#title        Molecular cloning of a human immunoglobulin heavy chain
              variable (V-H) region with anti-myelin-associated
              glycoprotein activity.
#accession    A60943
#status       not compared with conceptual translation
#molecule_type mRNA
#residues     1-151 #label DES
REFERENCE     Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.;
#authors      Alt, F.W.; Kabat, E.A.; Latov, N.
#journal      J. Neuroimmunol. (1990) 26:35-41
#title        Molecular cloning of a human immunoglobulin heavy chain
              variable (V-H) region with anti-myelin-associated
              glycoprotein activity.
#accession    A48165
#molecule_type mRNA
#residues     1-36, 'M', 38-62, 'AR', 67-151 #label DE2
#note         this sequence has been corrected in reference A60943
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        34-117
SUMMARY        #domain immunoglobulin homology #label IMM
              #length 151 #molecular-weight 16212 #checksum 3341
Query Match    74.5%; Score 686; DB 7; Length 151;
Best Local Similarity 72.8%; Pred. No. 3,22e-77;
Matches 91; Conservative 16; Mismatches 17; Indels 1; Gaps 1,
Db 20 qvqlvesggvvpqgsrlrscasgftfrygmhwrqagqgglewysvifdggtkyy 79
Qy 1 EVQLLESGGVGVPQGRSLRSLSCASGFTFTYGMHWRQAPCKGLEWVAGISFDGSSNQYY 60
Db 80 adsvkgrftisrdnsntlylqmslraedtavyycaard-f-fappn-wshidywqgtl 138
Qy 61 ADSVKGPFIIVSPNRPDTVFQMSLSLEDTAVYYCATEGSPFGSIKGRYYLENWQGTTL 120
Db 139 vtys 143
Qy 121 VTVSS 125
RESULT 3
ENTRY        S31117 #type complete
TITLE        Ig heavy chain - human
ORGANISM     #formal_name Homo sapiens #common_name man
DATE         02-Dec-1993 #sequence_revision 26-May-1995 #text_change
ACCESSIONS   S31117
REFERENCE     Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol,
#authors      M.J.D.; Vossen, J.M.; Schuurman, R.K.B.
#journal      Eur. J. Immunol. (1992) 22:247-251
#title        Restricted utilization of germ-line V(H)3 genes and short
              diverse third complementarity-determining regions (CD3) in
              human fetal B lymphocyte immunoglobulin heavy chain
              rearrangements.
#accession    S31117
#status       preliminary; nucleic acid sequence not shown.
              translation not shown
#molecule_type mRNA
#residues     1-122 #label RAA
#cross-references EMBL:X62967
#note         the nucleotide sequence was submitted to the EMBL Data
              Library, October 1991
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

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KEYWORDS      heterotetramer; immunoglobulin
FEATURE       15-98
SUMMARY       #domain immunoglobulin homology #label IMM
              #length 122 #molecular-weight 13664 #checksum 8348
Query Match    74.3%; Score 684; DB 7; Length 122;
Best Local Similarity 74.4%; Pred. No. 6.18e-77;
Matches 93; Conservative 17; Mismatches 12; Indels 3; Gaps 3;
Db 1 qvqlvesggvvpqgsrlrscasgftfrygmhwrqagqgglewysvifdggtkyy 60
Qy 1 EVQLLESGGVGVPQGRSLRSLSCASGFTFTYGMHWRQAPCKGLEWVAGISFDGSSNQYY 60
Db 61 adsvkgrftisrdnsntlylqmslraedtavyycaard-f-fappn-wshidywqgtl 117
Qy 61 ADSVKGRFIVSRDNRDTVFQMSLSLEDTAVYYCATEGSPFGSIKGRYYLENWQGTTL 120
Db 118 vtys 122
Qy 121 VTVSS 125
RESULT 4
ENTRY        M3HUAM #type complete
TITLE        Ig heavy chain V-III region (Cam) - human
ORGANISM     #formal_name Homo sapiens #common_name man
DATE         31-Aug-1980 #sequence_revision 23-Oct-1981 #text_change
ACCESSIONS   A02051
REFERENCE     Letman, D.W.; Putnam, F.W.
#authors      Proc. Natl. Acad. Sci. U.S.A. (1980) 77:3249-3244
#journal      Amino acid sequence of the variable region of a human mu
#title        chain; location of a possible J-H segment.
#cross-references MIM:81013859
#accession    A02051
#molecule_type protein
#residues     1-122 #label IEH
COMMENT       This mu chain was isolated from the plasma of a patient with
              macroglobulinemia.
GENETICS      GDB:IGHV#
#gene
#cross-references GDB:128528
#map_position 14q32.33-14q32.33
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin; pyroglutamic acid
FEATURE       15-98
SUMMARY       #domain immunoglobulin homology #label IMM
              #modified site pyroglutamic acid (Gln) #status
              experimental
              #disulfide_bonds #status predicted
              #length 122 #molecular-weight 13668 #checksum 7281
Query Match    74.2%; Score 683; DB 2; Length 122;
Best Local Similarity 67.2%; Pred. No. 8.57e-77;
Matches 84; Conservative 27; Mismatches 11; Indels 3; Gaps 2;
Db 1 qvqlvesggvvpqgsrlrscasgftfrygmhwrqagqgglewysvifdggtkyy 60
Qy 1 EVQLLESGGVGVPQGRSLRSLSCASGFTFTYGMHWRQAPCKGLEWVAGISFDGSSNQYY 60
Db 61 adsvkgrftisrdnsntlylqmslraedtavyycaard-f-fappn-wshidywqgtl 117
Qy 61 ADSVKGPFIIVSPNRPDTVFQMSLSLEDTAVYYCATEGSPFGSIKGRYYLENWQGTTL 120
Db 118 vtys 122
Qy 121 VTVSS 125
RESULT 5
ENTRY        E36005 #type complete
TITLE        Ig heavy chain V region (M7) - human

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ORGANISM      #formal_name Homo sapiens #common_name man
DATE          21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change
ACCESSIONS    E36005
REFERENCE      Schroeder Jr., H.W.; Wang, J.Y.
#authors      Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6146-6150
#journal      Preferential utilization of conserved immunoglobulin heavy
#title        chain variable gene segments during human fetal life.
#cross-references MUID:90349571
#accession    E36005
##status      preliminary
##molecule_type mRNA
##residues    1-122 ##label SCH
##cross-references GB:M34030
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE       15-98
SUMMARY       #domain immunoglobulin homology #label IMM
#length 122 #molecular-weight 13527 #checksum 530

Query Match 73.8%; Score 680; DB 7; Length 122;
Best Local Similarity 74.6%; Pred. No. 2.28e-76;
Matches 94; Conservative 17; Mismatches 10; Indels 5; Gaps 4;

Db 1 qvqlvsgggvvpqrsirlscasgffsfssyhmhwraqpqlgwvavlsyqsnkyy 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1 EVQLLESGGVPVQPGPSLPISCAASGFTFKYGMHWVPQAPGKGFVWAGISFGDSNGYY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61 adsvkgrfistrdskntlylqmslraedtavvyqard-rh-ss--swyygmdivwgggt 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ADSVKGRFIVSRDNGSPDVFVQLQMSLPLEDTAVVYCATGEGSPFGSIKGPVY-LENWQGT 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 117 tvtvs 122
   |||||
QY 120 LTVSS 125
   |||||

RESULT 6
ENTRY      M1HNGA      #type complete
TITLE      Ig heavy chain V-III region (Ga) - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       #sequence_revision 23-Oct-1981 #text_change 31-Dec-1996
ACCESSIONS A02052
REFERENCE   A02052
#authors    Florent, G.; Lehman, D.; Putnam, F.W.
#journal    Biochemistry (1974) 13:2482-2490
#title      The switch point in mu heavy chains of human IgM
            immunoglobulins.
#cross-references MUID:74175307
#accession  A02052
##molecule_type protein
##residues  1-122 ##label FLO
COMMENT     This chain was isolated from a Waldenström's macroglobulin.
GENETICS    #gene      GDB:IGHV6
#cross-references GDB:128528
#map_position 14q32.33-14q32.33
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin, pyroglutamic acid
FEATURE       15-98
SUMMARY       #domain immunoglobulin homology #label IMM
#length 122 #molecular-weight 13166 #checksum 7775

Query Match 73.7%; Score 679; DB 2; Length 122;
Best Local Similarity 64.0%; Pred. No. 3.16e-76;
Matches 80; Conservative 30; Mismatches 12; Indels 3; Gaps 1;

Db 1 qvzlvszgggavpqrslrscasgffsfssyhmhwraqpqlzwlslvsybgbbzyy 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY 1 EVQLLESGGVPVQPGPSLPISCAASGFTFKYGMHWVPQAPGKGFVWAGISFGDSNGYY 60
Db 61 adsvkgrfistrdskntlylqmslraedtavvyqard-rh-ss--swyygmdivwgggt 117
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ADSVKGRFIVSRDNGSPDVFVQLQMSLPLEDTAVVYCATGEGSPFGSIKGPVY-LENWQGT 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 118 vtiiss 122
   |||||
QY 121 VTISS 125
   |||||

RESULT 7
ENTRY      S36278      #type fragment
TITLE      Ig heavy chain V region (clone alpha-TU-23) - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
ACCESSIONS S36278
REFERENCE   S36256
#authors    Griffiths, A.D.; Walevski, M.; Marks, J.D.; Rye, T.M.;
            Embleton, M.J.; McGafferty, J.; Baier, M.; Holliger, K.P.;
            Gorlick, R.D.; Hughes-Jones, N.C.; Hoogenboom, H.P.; Winter,
            G.
#journal    EMBO J. (1993) 12:725-734
#title      Human anti-self antibodies with high specificity from phage
            display libraries.
#accession  S36278
##status      preliminary; nucleic acid sequence not shown
##molecule_type mRNA
##residues    1-120 ##label GPI
##cross-references EMBL:Z18430
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE       15-98
SUMMARY       #domain immunoglobulin homology #label IMM
#length 120 #checksum 7337

Query Match 73.5%; Score 677; DB 7; Length 120;
Best Local Similarity 72.6%; Pred. No. 6.07e-76;
Matches 90; Conservative 19; Mismatches 11; Indels 4; Gaps 4;

Db 1 qvzlvszgggavpqrslrscasgffsfssyhmhwraqpqlzwlslvsybgbbzyy 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1 EVQLLESGGVPVQPGPSLPISCAASGFTFKYGMHWVPQAPGKGFVWAGISFGDSNGYY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61 adsvkgrfistrdskntlylqmslraedtavvyqard-rh-ss--swyygmdivwgggt 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ADSVKGRFIVSRDNGSPDVFVQLQMSLPLEDTAVVYCATGEGSPFGSIKGPVY-LENWQGT 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 117 vtiiss 120
   |||||
QY 121 VTISS 124
   |||||

RESULT 8
ENTRY      S48797      #type complete
TITLE      Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
ACCESSIONS S48797
REFERENCE   S48797
#authors    Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
            submitted to the EMRL Data Library, October 1994
#description Molecular characterization of natural human anti-Sm
            autoantibodies.
#accession  S48797
##status      preliminary
##molecule_type mRNA
##residues    1-128 ##label MAH
##cross-references EMBL:Z46379
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

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KEYWORDS
FEATURE
15-98
SUMMARY
    heterotetramer; immunoglobulin
    #domain immunoglobulin homology #label IMM
    #length 128 #molecular-weight 14474 #checksum 9058
Query Match
Best Local Similarity 73.0%; Score 672; DB 7; Length 128;
Matches 94; Conservative 14; Mismatches 17; Indels 3; Gaps 1;

Db 1 qvqlvesggvvqgrslrscasgffsfssygmhwvraqpdkglewvavivdgsnkyy 60
QY 1 EVQLLESGGVSQVQPSRLSLRSCAASGFTFKYGMHWVRQAPGKGLWVAGISFDGSNQYY 60

Db 61 adsvkgrftisrdnsknltlylqmnslraedtavvyccardnyvssgyvyygmddvqg 120
QY 61 ADSVKGRFIVSRDNRDVFLOMSSLRLIEDTAVVYCATEGSPFGSIKGRYY---LENWGO 117

Db 121 gttvtvss 128
QY 118 GTLVTVSS 125

RESULT 9
ENTRY
TITLE
ORGANISM
DATE
    S31116 #type complete
    Ig heavy chain - human
    #formal_name Homo sapiens #common_name man
    02-Dec-1993 #sequence_revision 26-May-1995 #text_change
    30-May-1997
ACCESSIONS
REFERENCE
    S31116
    S31104
    Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol,
    M.J.D.; Vossen, J.M.; Schuurman, R.K.B.
    Eur. J. Immunol. (1992) 22:247-251
    Restricted utilization of germ-line V(H)3 genes and short
    diverse third complementarity-determining regions (CDR3) in
    human fetal B lymphocyte immunoglobulin heavy chain
    rearrangements.
    #accession S31116
    #status preliminary; nucleic acid sequence not shown,
    translation not shown
    #molecule_type mRNA
    #residues 1-118 #label RAA
    #cross-references EMBL:X62966
    #note the nucleotide sequence was submitted to the EMBL Data
    Library, October 1991
CLASSIFICATION
KEYWORDS
FEATURE
15-98
SUMMARY
    #superfamily immunoglobulin V region; immunoglobulin homology
    heterotetramer; immunoglobulin
    #domain immunoglobulin homology #label IMM
    #length 118 #molecular-weight 12778 #checksum 4374
Query Match
Best Local Similarity 72.7%; Score 670; DB 7; Length 118;
Matches 96; Conservative 15; Mismatches 7; Indels 7; Gaps 3;

Db 1 qvqlvesggvvqgrslrscasgffsfssygmhwvraqpdkglewvavivdgsnkyy 60
QY 1 EVQLLESGGVSQVQPSRLSLRSCAASGFTFKYGMHWVRQAPGKGLWVAGISFDGSNQYY 60

Db 61 adsvkgrftisrdnsknltlylqmnslraedtavvyccatdg---g-kaaf--diwqgqtm 113
QY 61 ADSVKGRFIVSRDNRDVFLOMSSLRLIEDTAVVYCATEGSPFGSIKGRYYLENWGOJTL 120

Db 114 vtvs 118
QY 121 VTVSS 125

RESULT 10
ENTRY
TITLE
ORGANISM
DATE
    G36005 #type complete
    Ig heavy chain V region (M74) - human
    #formal_name Homo sapiens #common_name man
    21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change

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16-Aug-1996
ACCESSIONS
REFERENCE
    G36005
    Schroeder Jr., H.W.; Wang, J.Y.
    Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6146-6150
    Preferential utilization of conserved immunoglobulin heavy
    chain variable gene segments during human fetal life.
    #cross-references MIMD:90349571
    #accession G36005
    #status preliminary
    #molecule_type mRNA
    #residues 1-121 #label SCH
    #cross-references GB:M34031
    #superfamily immunoglobulin V region; immunoglobulin homology
    heterotetramer; immunoglobulin
    #domain immunoglobulin homology #label IMM
    #length 121 #molecular-weight 13508 #checksum 6962
Query Match
Best Local Similarity 72.7%; Score 670; DB 7; Length 121;
Matches 93; Conservative 15; Mismatches 13; Indels 4; Gaps 3;

Db 1 qvqlvesggvvqgrslrscasgffsfssygmhwvraqpdkglewvavivdgsnkyy 60
QY 1 EVQLLESGGVSQVQPSRLSLRSCAASGFTFKYGMHWVRQAPGKGLWVAGISFDGSNQYY 60

Db 61 adsvkgrftisrdnsknltlylqmnslraedtavvyccardkdwg--a-lf-dywgqatl 116
QY 61 ADSVKGRFIVSRDNRDVFLOMSSLRLIEDTAVVYCATEGSPFGSIKGRYYLENWGOJTL 120

Db 117 vtvs 121
QY 121 VTVSS 125

RESULT 11
ENTRY
TITLE
ORGANISM
DATE
    S31674 #type fragment
    Ig heavy chain V region - human (fragment)
    #formal_name Homo sapiens #common_name man
    22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
    16-Aug-1996
ACCESSIONS
REFERENCE
    S31674
    S31785
    Guisnier, A.M.; Gauthier, L.; Boubli, L.; Fouqueray, M.;
    Tonnel, C.
    Submitted to the EMBL Data Library, June 1992
    Mechanisms that generate human immunoglobulin diversity
    operate from the 8th week of gestation in fetal liver.
    #accession S31674
    #status preliminary
    #molecule_type mRNA
    #residues 1-139 #label CUI
    #cross-references EMBL:214204
    #superfamily immunoglobulin V region; immunoglobulin homology
    heterotetramer; immunoglobulin
    #domain immunoglobulin homology #label IMM
    #length 139 #checksum 3756
Query Match
Best Local Similarity 72.2%; Score 670; DB 7; Length 139;
Matches 94; Conservative 15; Mismatches 11; Indels 5; Gaps 3;

Db 20 qvqlvesggvvqgrslrscasgffsfssygmhwvraqpdkglewvavivdgsnkyy 79
QY 1 EVQLLESGGVSQVQPSRLSLRSCAASGFTFKYGMHWVRQAPGKGLWVAGISFDGSNQYY 60

Db 80 adsvkgrftisrdnsknltlylqmnslraedtavvyccakqlf--fn-wf-dpwqatl 134
QY 61 ADSVKGRFIVSRDNRDVFLOMSSLRLIEDTAVVYCATEGSPFGSIKGRYYLENWGOJTL 120

Db 135 vtvs 139

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Query Match 121 VIVSS 125
Best Local Similarity 72.08; Score 663; DB 7; Length 133;
Matches 91: Conservative 16; Mismatches 16; Indels 2; Gaps 2;

RESULT 12
ENTRY S38493 #type fragment
TITLE Ig heavy chain - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
16-Aug-1995
ACCESSIONS S38493
REFERENCE S38498
#authors Marks, J.D.; Ouehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.; Hughes-Jones, N.C.; Winter, G.
#submission submitted to the EMBL Data Library, June 1993
#description Human antibody fragments specific for human blood group antigens from a phage display library.
#accession S38493
#status preliminary
#molecule_type DNA
#residues 1-123 #label MAP
#cross-references EMBL:223036
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 15-98
SUMMARY #domain immunoglobulin homology #label IMM
#length 123 #checksum 2856

Query Match 72.18; Score 664; DB 7; Length 123;
Best Local Similarity 73.08; Pred. No. 4.21e-74;
Matches 92: Conservative 12; Mismatches 12; Indels 2; Gaps 1;

Db 1 qvqlsgggvvgpgsrslscsaasgftfssygmhvwrgapkglewavvisydgskyy 60
1 EVQLLESGGAVGPGSRSLSCSAASGFTFKYGMHWVPAPKGLFWASISFTSSNAYY 60
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61 ADSVKGRFIVSRPNSTQVFIQMSLSRLRLETAIVYVCATEGSPFGSIKGYVLENWQQTG 120
119 vtvs 123
121 VIVSS 125

RESULT 13
ENTRY A49028 #type fragment
TITLE Ig heavy chain V-III region - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change
16-Aug-1994
ACCESSIONS A49028
REFERENCE A49028
#authors Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuurman, P.K.
#journal Eur. J. Immunol. (1993) 21:2355-2363
#title Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphoblastoid cell lines from X-linked agammaglobulinemia patients.
#cross-references MIM:92008140
#accession A49028
#status preliminary
#molecule_type mRNA
#residues 1-133 #label TIM
#cross-references NCBI:64471; NCBI:64470
#experimental_source X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
#note sequence extracted from NCI backbone
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 15-98
SUMMARY #domain immunoglobulin homology #label IMM
#length 133 #checksum 8516

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Best Local Similarity 76.08; Pred. No. 8.08e-74;
Matches 95: Conservative 14; Mismatches 8; Indels 8; Gaps 2;

Db 16 qvqlsgggvvgpgsrslscsaasgftfssygmhvwrgapkglewavvisydgskyy 75
1 EVQLLESGGAVGPGSRSLSCSAASGFTFKYGMHWVPAPKGLFWASISFTSSNAYY 60
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129 vtvs 132
121 VIVSS 125

RESULT 15
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TITLE Ig heavy chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Dec-1993 #sequence_revision 26-May-1995 #text_change
16-Aug-1995
ACCESSIONS S31112
REFERENCE S31104
#authors Paaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, R.K.B.
#journal Eur. J. Immunol. (1993) 23:247-251
#title Restricted utilization of germ-line V(H)3 genes and short diverse third complementarity-determining regions (CDR3) in human fetal B lymphocyte immunoglobulin heavy chain

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rearrangements.
#accession S31112
##status preliminary; nucleic acid sequence not shown;
translation not shown
##molecule_type mRNA
##residues 1-120 ##label RAA
##cross-references EMBL:X62961
##note the nucleotide sequence was submitted to the EMBL Data
Library, October 1991
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
heterotetramer; immunoglobulin
FEATURES
15-98
SUMMARY #domain immunoglobulin homology #label IMM
#length 120 #molecular-weight 12974 #checksum 8808

Query Match 71.8% Score 661; DB 7; Length 120;
Best Local Similarity 76.0% Pred No 1 12e-73;
Matches 95; Conservative 13; Mismatches 12; Indels 5; Gaps 3;

Db 1 qvqlvesggvgvqgrslrlscaasgftfssyamhwrrgapkglewvavisdgskyy 60
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Db 61 adsvkgrftlsrdnsksntlylqmslraedtavyycat-qvvv-vvaatdy---wggqtl 115
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Qy 61 ADSVKGFPIVSRDNRDTVFQMSLSRLIEDTAVYCATGSPFGSIKGRYYLENWGGGL 120

Db 116 vtvss 120
|||||
Qy 121 VTVSS 125

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Search completed: Tue Feb 24 07:09:52 1998
Job time : 14 secs.

MORRIS
***** (TM)

Release 2 ID John F. Collins, Biocomputing Research Unit
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Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:37:11 1998; Master time 2.42 Seconds
Tabular output not generated. 186.065 Million cell updates/sec

Title: >US-08-844-215-4
Description: (1-125) from US08844215.pep
Perfect Score: 921
Sequence: 1 EVQLLESGGCVGPGSLPL IKGPYLENKGQILIVSS 125

Scoring table: PAM 150
Gap 11

Searched: 56402 seqs, 5095871 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:58 10:59
10:PC192 11:PC193 12:PC194 13:PC195 14:PC196
Statistics: Mean 28.138; Variance 145.429; scale 0.193

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	669	72.6	119 7	US-08-331- Sequence 46, Applicat
2	665	72.3	120 7	US-07-942- Sequence 35, Applicat
3	657	71.3	141 6	US-08-259- Sequence 2, Applicatio
4	652	71.3	141 7	US-08-468- Sequence 2, Applicatio
5	652	70.8	125 7	US-08-478- Sequence 99, Applicati
6	650	70.6	125 11	PCT-US93-1 Sequence 5, Applicatio
7	650	70.6	125 11	PCT-US93-1 Sequence 5, Applicatio
8	647	70.2	125 11	PCT-US93-1 Sequence 1, Applicati
9	641	69.6	123 7	US-08-478- Sequence 31, Applicat
10	638	69.3	123 7	US-08-478- Sequence 94, Applicat
11	637	69.2	123 7	US-08-211- Sequence 141, Applicat
12	632	68.6	122 11	PCT-US93-0 Sequence 43, Applicat
13	630	68.4	122 11	PCT-US93-0 Sequence 14, Applicati
14	628	68.2	98 6	US-08-211- Sequence 118, Applicat
15	628	68.2	122 11	PCT-US93-0 Sequence 12, Applicati
16	627	68.1	125 7	US-07-942- Sequence 33, Applicati
17	625	67.9	142 7	US-08-305- Sequence 2, Applicatio
18	624	67.8	125 13	PCT-US95-0 Sequence 76, Applicati
19	624	67.8	125 13	US-08-276- Sequence 76, Applicati
20	621	67.4	125 13	PCT-US95-0 Sequence 72, Applicati
21	621	67.4	125 7	US-08-276- Sequence 72, Applicati
22	621	67.4	144 5	US-08-025- Sequence 2, Applicatio

US-08-844-215-4.ra1

Thu Feb 26 07:06:00 1998

CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 543-9600
 CC TELEFAX: (415) 543-5043
 CC INFORMATION FOR SEQ ID NO: 46:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 119 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS:
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC FEATURE:
 CC NAME/KEY: Protein
 CC LOCATION: 1..119
 CC OTHER INFORMATION: /note="Human fetal immunoglobulin
 CC OTHER INFORMATION: 56p1'CL Variable Heavy chain (V-H)"
 CC OTHER INFORMATION: 119 AA: 13279 MW: 79818 CN:
 CC SEQUENCE 119 AA: 13279 MW: 79818 CN:
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 CC Query Match 72.68; Score 669; DB 7; Length 119;
 CC Best Local Similarity 75.28; Pred No 1 80e-44;
 CC Matches 94; Conservative 16; Mismatches 9; Indels 6; Gaps 4;
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 CC Db 1 QVELVESGGVQVQGRSLRLSCAASGFTFSYAMHWYRQAPGKGLEWVAVISYDGSNKYY 60
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 CC ID US-07-942-245-35 STANDARD: PRT; 120 AA.
 CC AC xxxxxx
 CC XX 01-JAN-1900
 CC DT
 CC DE Sequence 35, Application US/07942245.
 CC XX Sequence 35, Application US/07942245.
 CC Patent No. 5639641
 CC GENERAL INFORMATION:
 CC APPLICANT: PEDERSEN, Jan T.
 CC APPLICANT: SEARLE, Stephen M.J.
 CC APPLICANT: REES, Anthony R.
 CC APPLICANT: POGUSKA, Michael A.
 CC APPLICANT: GUILD, Braydon C.
 CC TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
 CC TITLE OF INVENTION: ANTIBODIES
 CC NUMBER OF SEQUENCES: 522
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Sughrie, Mion, Zinn, Macpeak & Seas
 CC STREET: 2100 Pennsylvania Avenue, N.W.
 CC CITY: Washington
 CC STATE: D.C.
 CC COUNTRY: United States
 CC ZIP: 20037-3202
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: HP 9000/700 Workstation
 CC OPERATING SYSTEM: UNIX
 CC SOFTWARE: In house
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/07/942,245
 CC FILING DATE: 09-SEP-1992
 CC CLASSIFICATION: 530
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (202) 293-7050
 CC TELEFAX: (202) 293-7860

CC TELEX: 6491103
 CC INFORMATION FOR SEQ ID NO: 35:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 120 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE 120 AA: 13421 MW: 78517 CN:
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 CC Query Match 72.3%; Score 666; DB 7; Length 120;
 CC Best Local Similarity 74.2%; Pred. NO. 3.16e-44;
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 CC QY 117 VTSS 120
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 CC QY 121 VTSS 124
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 CC RESULT 3
 CC ID US-08-259-372A-2 STANDARD: PRT; 141 AA.
 CC AC xxxxxx
 CC XX 01-JAN-1900
 CC DT
 CC DE Sequence 2, Application US/08259372A.
 CC XX Sequence 2, Application US/08259372A
 CC Patent No. 5565354
 CC GENERAL INFORMATION:
 CC APPLICANT: Ostberg, Lars G.
 CC TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
 CC TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIG
 CC
 CC EN
 CC NUMBER OF SEQUENCES: 16
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend and Crew LLP
 CC STREET: Two Embarcadero Center, Eighth Floor
 CC CITY: San Francisco
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 94111-3834
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.10
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/259,372A
 CC FILING DATE: 14-JUN-1994
 CC CLASSIFICATION: 424
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/871,426
 CC FILING DATE: 21 APR-1992
 CC PRIOR APPLICATION DATA: US 07/676,036
 CC APPLICATION NUMBER: 27-MAR-1991
 CC FILING DATE: 27-MAR-1991
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/538,796
 CC FILING DATE: 15-JUN-1990
 CC PRIOR APPLICATION DATA: US 07/192,754
 CC APPLICATION NUMBER: 11-MAY-1988
 CC FILING DATE: 11-MAY-1988
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 06/925,196

US-08-844-215-4-rai

Thu Feb 26 07:06:00 1998

CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.30
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/478,039
 CC FILING DATE: 07-JUN-1995
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/379,072
 CC FILING DATE: 25-JAN-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/912,292
 CC FILING DATE: 10-JUL-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/856,281
 CC FILING DATE: 23-MAR-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/735,064
 CC FILING DATE: 25-JUL-1991
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Teskin Esq., Robin L.
 CC REGISTRATION NUMBER: 35,030
 CC REFERENCE/DOCKET NUMBER: 012712-160
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 703-836-6620
 CC TELEFAX: 703-836-2021
 CC INFORMATION FOR SEQ ID NO: 99:
 CC SEQUENCE CHARACTERISTICS:
 CC TYPE: amino acid
 CC LENGTH: 125 amino acids
 CC STRANDEDNESS: not relevant
 CC TOPOLOGY: not relevant
 CC MOLECULE TYPE: peptide
 CC POSITION IN GENOME:
 CC CHROMOSOME/SEGMENT: 18/2
 CC SEQUENCE 125 AA; 13543 MW; 93321 CN;
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 Best Local Similarity 69.8%; Pred. No. 4,32e-43;
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 QY 61 ADSVKGRFIVSRDNRSDTVFLQMSLRLEDTAVYYCATLSPSPSIFGYYIFHWPGQTLL 120
 Db 120 LVTVSS 125
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 ID PCT-US93-10555-6
 XX AC xxxxxx
 XX DT 01-JAN-1900
 XX DE Sequence 6, Application PC/TUS9310555.
 XX CC Sequence 6, Application PC/TUS9310555
 CC GENERAL INFORMATION:
 CC APPLICANT: SILVERMAN, GREGG J.
 CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
 CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
 CC THROUGH
 CC ATES TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERNATANT AND CONJUG
 CC TITLE OF INVENTION: THEREOF
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Juntas & Lubitz
 CC STREET: 1880 Century Park East - Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/10555
 CC FILING DATE: 29-OCT-1993
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Howells, Stacy L.
 CC REGISTRATION NUMBER: 34,842
 CC REFERENCE/DOCKET NUMBER: FD-2630
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 6:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 125 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC IMMEDIATE SOURCE:
 CC CLONE: RIV
 CC FEATURE:
 CC NAME/KEY: Peptide
 CC LOCATION: 1,125
 CC SEQUENCE 125 AA; 13612 MW; 20992 CN;
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 Best Local Similarity 68.8%; Pred. No. 6,27e-44;
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 Db 61 VDSVKGRFTISPDOSKNTLYLQMSLRADETALYYCAKLTAAAGSFITDTYGMWQGTLL 120
 QY 61 ADSVKGRFIVSRDNRSDTVFLQMSLRLEDTAVYYCATLSPSPSIFGYYIFHWPGQTLL 120
 Db 121 VTVSS 125
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 RESULT 7
 ID PCT-US93-10555-5 STANDARD: PRT: 125 AA.
 XX AC xxxxxx
 XX DT 01-JAN-1900
 XX DE Sequence 5, Application PC/TUS9310555.
 XX CC Sequence 5, Application PC/TUS9310555
 CC GENERAL INFORMATION:
 CC APPLICANT: SILVERMAN, GREGG J.
 CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
 CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
 CC THROUGH
 CC ATES TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERNATANT AND CONJUG
 CC TITLE OF INVENTION: THEREOF

CC NUMBER OF SEQUENCES: 51
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Jubes & Lubitz
CC STREET: 1880 Century Park East - Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/10555
CC FILING DATE: 29-OCT-1993
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Howells, Stacy L.
CC REGISTRATION NUMBER: 34,842
CC REFERENCE/DOCKET NUMBER: PD-2630
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 125 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: KIM
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..125
CC SEQUENCE 125 AA; 13612 MW; 90692 CN;

Query Match 70.6%, Score 650, DE 11, Length 125;
Best Local Similarity 68.8%, Pred No 6, 27e-43;
Matches 86; Conservative 20; Mismatches 19; Indels 0; Gaps 0;

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Db 61 VDSVKGRTISPNKNTLYLQWNSLPARTAIYYCAKISTAASGPTFTTYGMWQGTTL 120
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XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 1, Application PCT/US93/10555.
XX CC Sequence 1, Application PCT/US93/10555
XX CC GENERAL INFORMATION:
CC APPLICANT: SILVERMAN, GREGG J.
CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
CC THROUGH
CC TITLE OF INVENTION: VACCINATION WITH A P-CELL SUPEROPTIMIZED AND CONJUG
CC ATES
CC TITLE OF INVENTION: THEREOF

CC NUMBER OF SEQUENCES: 51
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Jubes & Lubitz
CC STREET: 1880 Century Park East - Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/10555
CC FILING DATE: 29-OCT-1993
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Howells, Stacy L.
CC REGISTRATION NUMBER: 34,842
CC REFERENCE/DOCKET NUMBER: PD-2630
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 125 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: 18/2
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..125
CC SEQUENCE 125 AA; 13454 MW; 94507 CN;

Query Match 70.2%, Score 647, DE 11, Length 125;
Best Local Similarity 69.9%, Pred No 1, 10e-42;
Matches 89; Conservative 19; Mismatches 19; Indels 2; Gaps 2;

Db 1 EVQLVESGGGVVQPGSSLRISCAASGPTFTSSYAMSWVQAPKGLWVSAISGSGSTYY 60
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QY 1 EVQLVESGGGVVQPGSSLRISCAASGPTFTKTYGMHWVWQAPKGLWVAVMSYSINRIY 60
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Db 61 ADSVKGRTISPNKNTLYLQWNSLPARTAIYYCAKISTAASGPTFTTYGMWQGTTL 119
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QY 61 ADSVKGRTIVSRDNRSDIVFLQWSSLPLEDTAVYYCATGSPFGSIKGRYILENWSQGT 119
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Db 120 LTVSS 125
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QY 120 LTVSS 125

RESULT 9
ID PCT-US93-07832-21 STANDARD PPT: 122 AA
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 21, Application PCT/US93/07832.
XX CC Sequence 21, Application PCT/US93/07832
XX CC GENERAL INFORMATION:
CC APPLICANT: Genentech, Inc.
CC TITLE OF INVENTION: Immunoglobulin Variants
CC NUMBER OF SEQUENCES: 40
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco

US-08-844-215-4.ra1

Thu Feb 26 07:06:00 1998

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CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM.
CC MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/07832
CC FILING DATE: 19930820
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/715272
CC FILING DATE: 14-JUN-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/05126
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/934373
CC FILING DATE: 21-AUG-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME:
CC REGISTRATION NUMBER:
CC REFERENCE/DOCKET NUMBER: 709P2PCT
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE:
CC TELEFAX: 415/952-9881
CC TELEX: 910/371-7168
CC INFORMATION FOR SEQ ID NO: 21:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 122 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC SEQUENCE 122 AA: 13077 MW: 86439 CN;

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Best Local Similarity 72.0%; Pred. No. 3.37e-42;
Matches 90; Conservative 16; Mismatches 16; Indels 3; Gaps 3;

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Qy 1 EVQLVESGGGVQPGGSLRLSCAASGFTFKYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
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Dd 61 ADSVKGRFTISRDNSNTLYLQMSLRAEDTAVYYCARGVY-SLSC-LY-DYWGSGTL 117
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Qy 61 ADSVKGRFIVSRDNRSDTAVYYCARGVY-SLSC-LY-DYWGSGTL 117
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Dd 118 VTVSS 122
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Qy 121 VTVSS 125
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RESULT 10
ID US-08-478-039-94 STANDARD: PRT: 123 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 94, Application US/08478039
XX CC Sequence 94, Application US/08478039
XX CC Patent No. 5681722
XX CC GENERAL INFORMATION:
XX CC APPLICANT: Newman, Roland A.
XX CC APPLICANT: Hanna, Nabii
XX CC APPLICANT: Raab, Ronald W.
XX CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
XX CC NUMBER OF SEQUENCES: 114
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: BURNS, DOANE, SWEETKEP & MATHIS
XX CC STREET: 699 Prince St.

CC CITY: Alexandria
CC STATE: VA
CC COUNTRY: USA
CC ZIP: 22313-1404
CC COMPUTER READABLE FORM.
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.40
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/478,039
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/379,072
CC FILING DATE: 25-JAN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/912,292
CC FILING DATE: 10-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/856,281
CC FILING DATE: 23-MAR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/735,064
CC FILING DATE: 25-JUL-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Teskin Esq., Robin L.
CC REGISTRATION NUMBER: 35,030
CC REFERENCE/DOCKET NUMBER: 012712-160
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 703-836-6620
CC TELEFAX: 703-836-2021
CC INFORMATION FOR SEQ ID NO: 94:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 123 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: not relevant
CC MOLECULE TYPE: peptide
CC POSITION IN GENOME:
CC CHROMOSOME/SEGMENT: RF 1S2
CC SEQUENCE 123 AA: 13515 MW: 82958 CN;

Query Match 69.3%; Score 638; DB 7; Length 123;
Best Local Similarity 69.1%; Pred. No. 5.89e-42;
Matches 85; Conservative 20; Mismatches 17; Indels 1; Gaps 1;

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Qy 1 EVQLVESGGGVQPGGSLRLSCAASGFTFKYGMHWVRQAPGKGLEWVAGISFDGSNQYY 60
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Dd 61 ADSVKGRFTISRDNSNTLYMGMSLRAEDTAVYYCARDRVAVYASVFFIDSPDIWGQT 120
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Qy 61 ADSVKGRFIVSRDNRSDTAVYYCARDRVAVYASVFFIDSPDIWGQT 119
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Qy 120 LVT 122
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RESULT 11
ID US-08-211-202-141 STANDARD: PRT: 116 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 141, Application US/08211202.
XX CC Sequence 141, Application US/08211202
XX CC Patent No. 556332
XX CC GENERAL INFORMATION:
XX CC APPLICANT: HOOGENBOOM, Hendricus Renorus Jacobus Mattheus

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CC APPLICANT: BAIER, Michael
CC APPLICANT: JESPER, Laurent Stephane Anne Therese
CC APPLICANT: WINTER, Gregory Paul
CC TITLE OF INVENTION: Production of chimeric antibodies - a
CC TITLE OF INVENTION: combinatorial approach
CC NUMBER OF SEQUENCES: 144
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
CC ADDRESSEE: Borun
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606-6402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1 0, Version #1 25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/211,202
CC FILING DATE: 23-SEP-1992
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GR 9120252.3
CC FILING DATE: 23-SEP-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GR 9120377.8
CC FILING DATE: 25-SEP-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GR 9206318.9
CC FILING DATE: 24-MAR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GR 9206372.5
CC FILING DATE: 24-MAR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/FR92/00883
CC FILING DATE: 15-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: David W. Clough
CC REGISTRATION NUMBER: 36 107
CC REFERENCE/DOCKET NUMBER: 28111/31950
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312-474-6300
CC TELEFAX: 312-474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 141:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 116 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 116 AA; 12678 MW; 72426 CN;
SQ
Query Match 69.2%; Score 637; DB 6; Length 116;
Best Local Similarity 73.7%; Pred. No. 7.10e-42;
Matches 87; Conservative 16; Mismatches 13; Indels 2; Gaps 2;
Db 1 QVQLVESGGGVVQPGSPSLFSCASGFTFESSYAMHWVQAPGKGLEWVAIVSYDGSNKYY 60
QY 1 EVQLLESGGAVGQPGSPSLFSCASGFTFKTYGMHWVQAPGKGLEWVAIGISFDGSNQY 60
Db 61 ADSVKGRTTSPENSKNTLYLQMSLRARLTAVVYQAS-QP-VCSGGSGSPFFVWS-QE 116
QY 61 ADSVKGRTVSRDNPOTVFLQMSLRPLEDTAVVYCATGSPFGSIKGPYYLENWGG 118
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ID PCT-US93-08435-43 STANDARD: PRT: 122 AA.
XX
AC xxxxxx
XX 01-JAN-1900
DT

XX Sequence 43, Application PC/TUS9308435.
DE
XX Sequence 43, Application PC/TUS9308435.
XX GENERAL INFORMATION:
CC APPLICANT: SmithKline Beecham, Corporation
CC APPLICANT: U.S. Government, Secretary of
CC APPLICANT: the Navy
CC APPLICANT: U.S. Government, Secretary of
CC APPLICANT: the Army
CC TITLE OF INVENTION: Novel Antibodies for Conferring Passive
CC TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
CC NUMBER OF SEQUENCES: 61
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Howson and Howson
CC STREET: Box 457, 321 Norristown Road
CC CITY: Spring House
CC STATE: PA
CC COUNTRY: USA
CC ZIP: 19477
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/08435
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/941,654
CC FILING DATE: 03-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Bak, Mary E.
CC REGISTRATION NUMBER: 31,215
CC REFERENCE/DOCKET NUMBER: SRC P50107
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (215) 540-9200
CC TELEFAX: (215) 540-5818
CC INFORMATION FOR SEQ ID NO: 43:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 122 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 122 AA; 13313 MW; 87403 CN;
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Query Match 68.5%; Score 632; DB 11; Length 122;
Best Local Similarity 71.2%; Pred. No. 1.80e-41;
Matches 89; Conservative 15; Mismatches 18; Indels 3; Gaps 3;
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QY 1 EVQLLESGGGVVGQPGSPSLPUSCAASGFTFKIYGMHWVQAPGKGLEWVAGISFDGSNQY 60
Db 61 PQTVTGRTTISEKSNKNTLYLQMSLRPAEDTAVVYQASLIY-VG-VYLG-YAMLYWQGITL 117
QY 61 ALSVKGRTVSRDNPOTVFLQMSLRPLEDTAVVYQASLIY-AIE-SPFGSIKGPYYLENWQGITL 120
Db 118 VTSS 122
QY 121 VTSS 125
RESULT 13
ID PCT-US93-08435-14 STANDARD: PRT: 122 AA.
XX
AC xxxxxx
XX 01-JAN-1900
DT Sequence 14, Application PC/TUS9308435.
XX

US-08-844-215-4-rai

Thu Feb 26 07:06:00 1998

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CC Sequence 14, Application PC/TUS9308435
CC GENERAL INFORMATION:
CC APPLICANT: SmithKline Beecham, Corporation
CC APPLICANT: U. S. Government, Secretary of
CC APPLICANT: the Navy
CC APPLICANT: U. S. Government, Secretary of
CC APPLICANT: the Army
CC TITLE OF INVENTION: Novel Antibodies for Conferring Passive
CC TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
CC NUMBER OF SEQUENCES: 61
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Howson and Howson
CC STREET: Box 457, 321 Norristown Road
CC CITY: Spring House
CC STATE: PA
CC COUNTRY: USA
CC ZIP: 19477
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/08435
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GB 9120252.3
CC FILING DATE: 23-SEP-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GB 9120377.8
CC FILING DATE: 25-SEP-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GB 9206318.9
CC FILING DATE: 24-MAR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GB 9206372.6
CC FILING DATE: 24-MAR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/GB92/00883
CC FILING DATE: 15-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: David W. Clough
CC REGISTRATION NUMBER: 36,107
CC REFERENCE/DOCKET NUMBER: 28111/31960
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312-474-6300
CC TELEFAX: 312-474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 118:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 98 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 98 AA; 10838 MW; 50043 CN;
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CC Query Match 68.4%; Score 630; DB 11; Length 122;
CC Best Local Similarity 70.4%; Pred. No. 2.62e-41;
CC Matches 88; Conservative 16; Mismatches 18; Indels 3; Gaps 3;
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CC QY 1 EVOLLESGGVVQVQFGRSLRLSCAASGFTFKYGMHVRQAPGKLEWVAGISFDGSGNOYY 60
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CC Db 61 PTVTVGRFTISRDNSKNTLYIQMNSLRLEDYAVYCAALIV-YG-YDG-YAMDYWGQGITL 117
CC QY 61 ADSVKGRFIVSPDNRSDPTVFLQMSSRLRLSDYAVYCAALIV-YG-YDG-YAMDYWGQGITL 120
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CC Db 118 VTVSS 122
CC QY 121 VTVSS 125
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CC RESULT 14
CC ID US-08-211-202-118 STANDARD: PPT: 98 AA.
CC XX
CC AC xxxxxx
CC XX
CC DT 01-JAN-1900
CC XX
CC DE Sequence 118, Application US/08211202.
CC XX
CC CC Sequence 118, Application US/08211202
CC CC Patent No. 5565332
CC CC GENERAL INFORMATION:

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CC APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Mattheus
CC APPLICANT: BAIER, Michael
CC APPLICANT: JESPER, Laurent Stephane Anne Therese
CC APPLICANT: WINTER, Gregory Paul
CC TITLE OF INVENTION: Production of chimeric antibodies - a
CC TITLE OF INVENTION: combinatorial approach
CC NUMBER OF SEQUENCES: 144
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
CC ADPESSEE: Borun
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606-6402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/211,202
CC FILING DATE: 23-SEP-1992
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GB 9120252.3
CC FILING DATE: 23-SEP-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GB 9120377.8
CC FILING DATE: 25-SEP-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GB 9206318.9
CC FILING DATE: 24-MAR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GB 9206372.6
CC FILING DATE: 24-MAR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/GB92/00883
CC FILING DATE: 15-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: David W. Clough
CC REGISTRATION NUMBER: 36,107
CC REFERENCE/DOCKET NUMBER: 28111/31960
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312-474-6300
CC TELEFAX: 312-474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 118:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 98 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 98 AA; 10838 MW; 50043 CN;
CC
CC Query Match 68.2%; Score 628; DB 6; Length 98;
CC Best Local Similarity 83.5%; Pred. No. 3.80e-41;
CC Matches 81; Conservative 11; Mismatches 5; Indels 0; Gaps 0;
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CC QY 1 EVQLLESGGVVQVQFGRSLRLSCAASGFTFKYGMHVRQAPGKLEWVAVISYDGSNKYY 60
CC
CC Db 61 ADSVKGRFTISRDNSKNTLYIQMNSLRLEDYAVYCA 97
CC QY 61 ADSVKGRFIVSPDNRSDPTVFLQMSSRLRLSDYAVYCA 97
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CC RESULT 15
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CC XX
CC AC xxxxxx
CC XX

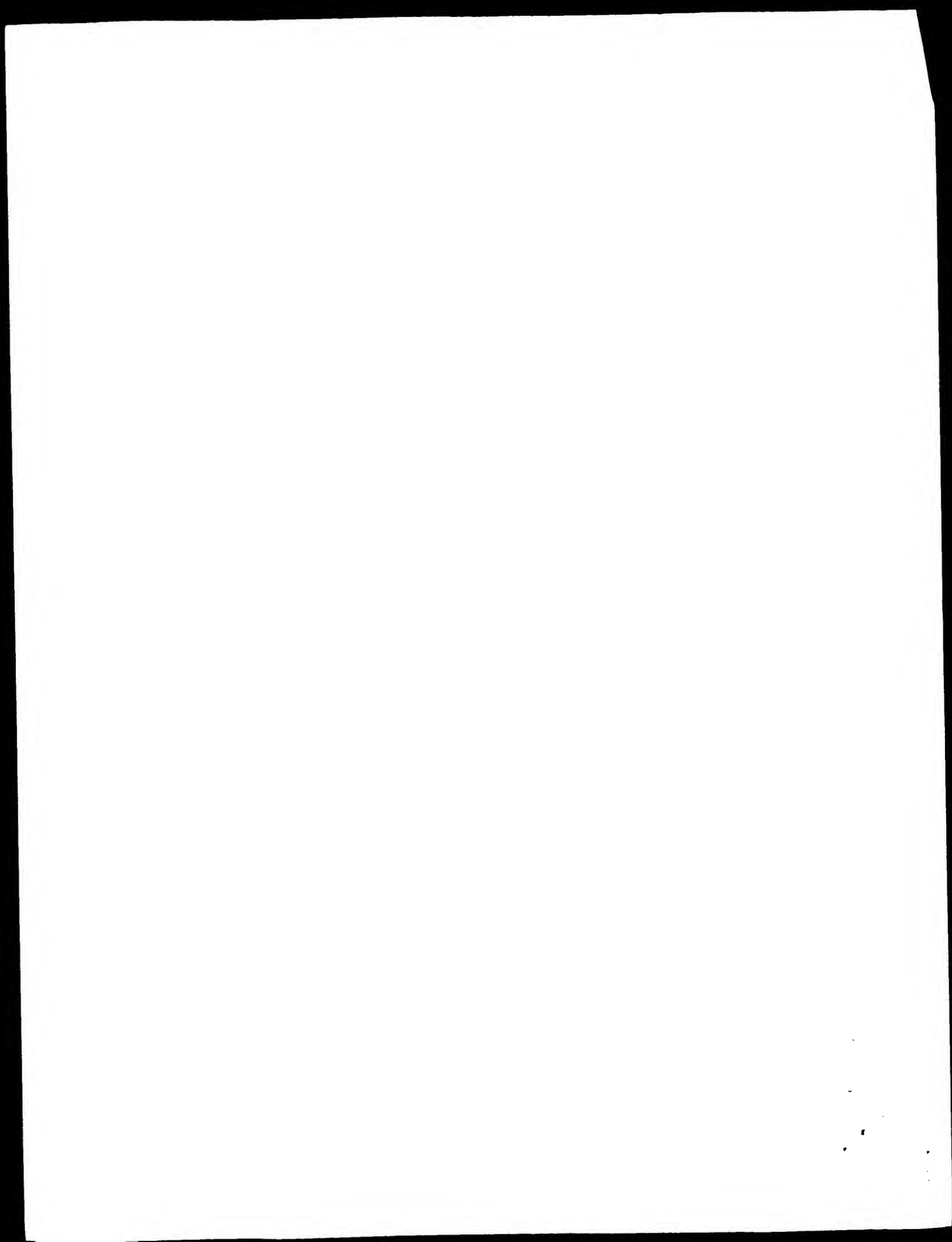
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DT 01-JAN-1900
XX
DE
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Sequence 12, Application PC/TUS9308435.
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Sequence 12, Application PC/TUS9308435
GENERAL INFORMATION:
CC APPLICANT: SmithKline Beecham, Corporation
CC APPLICANT: U. S. Government, Secretary of
CC APPLICANT: the Navy
CC APPLICANT: the Navy
CC APPLICANT: U. S. Government, Secretary of
CC APPLICANT: the Army
CC TITLE OF INVENTION: Novel Antibodies for Confering Passive
CC TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
CC NUMBER OF SEQUENCES: 61
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Howson and Howson
CC STREET: Box 457, 321 Norristown Road
CC CITY: Spring House
CC STATE: PA
CC COUNTRY: USA
CC ZIP: 19477
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC Compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/08435
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/941,654
CC FILING DATE: 09-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Bak, Mary E.
CC REGISTRATION NUMBER: 31,215
CC REFERENCE/DOCKET NUMBER: SEC P50107
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (215) 540-9200
CC TELEFAX: (215) 540-5818
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 122 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 122 AA; 13370 MW; 87746 CN;
SQ
Query Match 68.2%; Score 628; DB 11; Length 122;
Best Local Similarity 70.4%; Pred. No. 3,80e-41;
Matches 88; Conservative 15; Mismatches 19; Indels 3; Caps 3;
Db 1 EVOLLESGGIVQPGSLRISCAASGFTFSSVAMSVVPAQPKGLEWVSISDGGSYTY 60
QY 1 EVOLLESGGGVVQPSRLSRUSCAASGFTFKTGMHWVQAPKGLEWVAGISFDGSGNY 60
Db 61 PDVTIGRTTISPDNSKNTLYLQWNSLPARETAVVYCAKLIV-YR-YDQ-YAMDYWQGIT 117
QY 61 ADSVKGRFIVSPNSRDTVFLQWSSLPLEDTAVVYCATGEGSPFGSIKPYVLEWQGIT 120
Db 118 VTVSS 122
QY 121 VTVSS 125

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Search completed: Tue Feb 24 07:37:23 1998
Job time : 12 secs.



MIQE

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligentics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:10:11 1998; MasPar time 7.49 Seconds
231.859 Million cell updates/sec

Tabular output not generated.

Title: >US-08-844-215-4
Description: (1-125) from US08844215.pep
Perfect Score: 921
Sequence: 1 EVOLLESGGVGVGPGRSLRL

Scoring table: PAM 150
Gap 11

Searched: 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq30
1 part: 2 part2 3 part3 4 part4 5 part5 6 part6 7 part7
8 part8 9 part9 10 part10 11 part11 12 part12 13 part13
14 part14 15 part15 16 part16 17 part17 18 part18
19 part19 20 part20 21 part21 22 part22 23 part23

Statistics: Mean 30.277; Variance 155.246; scale 0.195

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	690	74.9	132	7	R38161	Sequence of the heavy
2	681	73.9	133	23	W15531	Anti-melanoma antibody
3	680	73.8	506	2	P12134	OPF 3 of 489 human MA
4	677	73.5	123	23	W15534	Anti-TGF beta-1 scfv
5	674	73.2	141	13	R75393	Anti-interleukin-1a1
6	669	72.6	119	19	R95216	Human foetal immunogl
7	668	72.5	123	23	W15535	Anti-TGF beta-1 scfv
8	666	72.3	115	4	P23571	Heavy chain VH3.5 fro
9	665	72.3	120	17	P52064	Heavy chain variable
10	657	71.3	141	19	W01522	Monoclonal antibody f
11	657	71.3	141	23	W24984	Monoclonal antibody p
12	653	70.9	140	23	W13524	Anti-human PBP HAM-R
13	651	70.7	143	9	P54047	Sequence of the VH re
14	650	70.6	156	9	P54788	SpA-reactive IgM heav
15	650	70.6	156	9	P54789	SpA-reactive IgM heav
16	649	70.5	123	22	W15536	Anti-TGF beta-1 scfv
17	639	69.4	111	2	P12275	Anti-human PBP HAM-R
18	638	69.3	124	23	W15537	Anti-melanoma antibod
19	638	69.3	125	9	P54784	SpA-reactive IgM heav
20	638	69.3	140	14	P84480	Anti-human IL-4 human

21	638	69.3	467	14	R80617	Anti-human IL-4 human
22	630	59.1	126	5	P29746	Heavy chain variable
23	624	59.8	117	12	R65321	Human immunoglobulin
24	623	59.7	142	6	R21534	M4H7 MAB heavy chain
25	622	59.6	122	9	P50315	Humanized heavy chain
26	621	59.5	126	7	R38613	KOL heavy chain
27	620	59.4	122	9	P50312	Humanized heavy chain
28	620	59.3	122	23	W15533	Anti-melanoma antibody
29	620	59.3	459	8	R42056	Human anti-HBs heavy
30	620	59.2	112	2	P12274	Anti-human PBP PEG-A
31	620	59.2	117	23	W15533	Anti-TGF beta-2 scfv
32	620	59.2	122	9	P50311	Humanized heavy chain
33	620	59.1	121	3	R13182	Variable region of u
34	620	59.1	121	10	P56234	162-109/112-61/h1-25
35	620	59.0	115	23	W15532	Anti-TGF beta-2 scfv
36	620	59.0	123	22	W08582	Human antibody C4.1 h
37	620	59.0	142	23	W22511	64-863 antibody H586
38	620	59.0	122	6	R30773	Consensus humanised m
39	620	59.0	125	10	R54208	Anti-HIV gp120 immuno
40	620	59.0	125	19	W01355	VH region of HIV neut
41	620	59.0	140	8	R41469	MAB 25D2 humanised be
42	620	59.0	116	6	R34286	Human TNP binding ant
43	620	59.0	125	19	W01251	VH region of HIV neut
44	620	59.0	125	10	R54248	Anti-HIV gp120 immuno
45	620	59.0	125	4	P29745	Recombinant heavy cha

ALIGNMENTS

RESULT 1
ID R38161 standard; Protein: 192 AA.
AC R38161:
DE 01-OCT-1993 (first entry)
DE Sequence of the heavy chain variable region (VH) of human
DE immunoglobulin G3 (19G3) produced by transformed human B-cell line
DE 88BV59, ATCC CRL 10624.
DE B-cell; immunoglobulin g; cancer; tumour.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..113
FT /label=VAR
FT /note="1st AA is denoted AA#1"
FT Region 31..49
FT /label= CDR 1
FT Region 50..94
FT /label= CDR 2
FT Region 95..111
FT /label= CDR 3
FT Region 112..223
FT /label= CH 1
FT Region 224..238
FT /label= Hinge
FT Region 239..242
FT /label= Fab'
PN FP-546634-A
PD 16-JUN-1993.
PF 09-DEC-1992; 203827.
PF 13-DEC-1991; US-887300.
PA (ALKU) AKZO NV
PI Crichton VZ, Haspel MV, Kobrin BJ;
DP WFI 93-196019/24.
DE N-TSDE, Q43772.
DE Transformed human B-cell line for monoclonal antibody prodn. for
DE cancer diagnosis - prepd from peripheral blood B-cells of cancer
DE patients actively immunised with atollous tumour antigen, for
DE treating cancers
PS Claim 5, Fig 2, 18pp, English.
CC Q43772 encodes the complete heavy chain from the leader through AAs
CC 242. 88BV59 uses VHIII and a D region which may have resulted from
CC intra-D-D recombination and/or gene conversion along with somatic
CC mutation. It is radically different from any germ line D region. It
CC utilises germ line JH3 it is of note that a cysteine at AA posn 50
CC (AA No. 78 in R38161) is present within the 88BV59 VH. No other

KW post myocardial infarction; post-angioplasty restenosis;
 KW scleroderma; vascular disease; cataract; glaucoma; scarring;
 KW glomerulonephritis; osteoporosis; immune disease; inflammation;
 KW rheumatoid arthritis; macrophage deficiency disease;
 KW macrophage pathogen infection; therapy.
 OS Homo sapiens.
 PN CB230521-A
 PD 23-APP-1997
 PF 07-OCT-1996; 020920
 PR 19-JAN-1996; GB-001081.
 PR 06-OCT-1995; GB-020486.
 PA (CAMEL) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Bacon L, Green JA, Jackson PH, Johnson KS, Pope AP.
 PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ.
 PI Wilton AJ.
 DR WPI: 97-215360/20.
 DR N-PSDB: T60380.
 PT Agent contg. antigen-binding domain of human antibody to transforming growth factor beta 1 or 2 - and nucleic acid encoding it, used to neutralise effects of TGF- α for control of fibrosis, immune and inflammatory disease
 PT Claim 16, Fig 1a(i), 18app. English.
 PS This polypeptide sequence comprises the VH domain of human scFv antibody 152 (also known as 7A3), which is specific for transforming growth factor (TGF) beta-1. It is encoded by a gene (T60380) isolated from a peripheral blood lymphocyte library. The antigen-binding domains of human antibodies (see W15522-40) to TGF beta-1 and/or beta-2 can be used to counter the adverse effects of TGF beta, such as (i) promotion of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis, arterial injury, proliferative retinopathy, retinal detachment, adult respiratory distress syndrome, liver cirrhosis, post myocardial infarction, post-angioplasty restenosis, scleroderma, vascular disorders, cataract, glaucoma, or esp. neural scarring and glomerulonephritis, also (not claimed) osteoporosis), or (ii) immune and inflammatory diseases (rheumatoid arthritis, macrophage deficiency diseases or macrophage pathogen infection). Nucleic acids encoding human antibody VH and VL can be used for prodn. of recombinant antigen-binding domains. These are highly specific, have low dissociation constants (pref. less than 5 nM) and low IC50s for neutralisation.
 SQ Sequence 123 AA.

Query Match 73.5%; Score 677; DB 23; Length 123;
 Best Local Similarity 73.6%; Pred. No. 1,30e-44;
 Matches 92; Conservative 16; Mismatches 15; Indels 2; Gaps 2;
 Db 1 qqlvsgggvqprslscasagffssvqmbwvraopkglewravisdgskyy 60
 QY 1 EVOLLESGGGVQPGSPSLSCASAGFFFTKTYGSMHWVQAPKGLWVAGISFDGSGNY 60
 Db 61 adsvkarftisrdnsKntlylgmslraedatavvycaqtge-ysgydsag-vdvwgkatt 118
 QY 61 AUSVKGFVFSVNSPSTVFLWSSLPLEDAVYVYVATGSPSPGSKGPPYLENWGGTLL 120
 Db 119 vtvs 123
 QY 121 VTVSS 125

RESULT 5
 ID R75393 standard: Protein: 141 AA.
 AC R75393;
 DT 04-NOV-1995 (first entry)
 DE Anti-interleukin-1-alpha human monoclonal antibody VH segment.
 KW Monoclonal antibody; interleukin-1-alpha; cytokines;
 KW antiinflammatory; prophylactic; therapeutic.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "signal peptide"
 FT Region 20..49
 FT /note= "Framework (FP) 1 (-1 to -30)"
 FT

FT /note= "CDR 1 (+31 to +35)"
 FT Region 55..68
 FT /note= "FR 2 (+36 to +49)"
 FT Region 54..85
 FT /note= "CDR 2 (+50 to +66)"
 FT Region 86..117
 FT /note= "FR 3 (+67 to +98)"
 FT Region 118..129
 FT /note= "CDR 3 (+99 to +110)"
 FT Region 130..141
 FT /note= "JH 1 (+111 to +122)"
 PN WO9514780-A.
 PD 01-JUN-1995.
 PF 21-NOV-1994; 013188
 PR 23-NOV-1993; EP-402846.
 PA (SCHE) SCHERING-PLOUGH.
 PI Ranchereau J, Djossou O, Fossiez F, Garonne P;
 DP WPI: 95-206937/27.
 DP N-PSDB: Q87236
 PT Human monoclonal antibody against a human cytokine - used to mfr a medicament to treat inflammation.
 PS Claim 7; Page 44-45; 70pp; English.
 CC The sequence represents the variable heavy chain segment of a human monoclonal antibody (HuMab) against interleukin-1-alpha. The Mab is of subclass IgG4 and binds to lymphokines/monokines with an affinity of 10(9)/M. The Mab or fragment (Fv, single-chain Fv, Fab or Fab') 2) is used in the treatment of inflammation e.g. rheumatoid arthritis, osteoarthritis and inflammatory bowel diseases, and in the treatment of psoriasis, allergic shock, graft vs host disease and tumours. The Mab or fragment can also be used for diagnosis.
 SQ Sequence 141 AA.
 Query Match 73.2%; Score 674; DB 13; Length 141;
 Best Local Similarity 73.6%; Pred. No. 2.29e-44;
 Matches 92; Conservative 15; Mismatches 15; Indels 3; Gaps 2;
 Db 20 qqlvsgggvqprslscasagffssvqmbwvraopkglewravisdgskyy 79
 QY 1 EVOLLESGGGVQPGSPSLSCASAGFFFTKTYGSMHWVQAPKGLWVAGISFDGSGNY 60
 Db 80 aevskarftisrdnsKntlylgmslraedatavvycaqtge-ysgydsag-vdvwgkatt 176
 QY 61 AUSVKGFVFSVNSPSTVFLWSSLPLEDAVYVYVATGSPSPGSKGPPYLENWGGTLL 120
 Db 137 vtfs 141
 QY 121 VTVSS 125

RESULT 6
 ID R95216 standard: Protein: 119 AA.
 AC R95216;
 DT 16-DEC-1996 (first entry)
 DE Human foetal immunoglobulin 56p1'c1 variable heavy chain.
 KW Antibody; fusion protein; single chain; inhibition; tumour;
 KW diagnosis; detection; imaging; immunotoxin; targeting; assay;
 KW immunoassay; Lewis(Y) carbohydrate antigen.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 31..35
 FT /label= CDR 1.
 FT Domain 50..66
 FT /label= CDR 2.
 FT Domain 99..108
 FT /label= CDR 3.
 PN WO9613594-A1.
 PD 09-MAY-1996.
 PF 26-OCT-1995; 013811.
 PR 28-OCT-1994; US-331398.
 PR 28-OCT-1994; US-331396.
 PR 28-OCT-1994; US-331397.

Claim 16: Fig 1a(ii): 184pp: English.
This polypeptide comprises the VH domain of human scv antibody 3LG5, which is specific for transforming growth factor (TGF)- β 1. It is encoded by a gene (760381) isolated from a large single chain Fv library. The antigen-binding domains of human antibodies (see W5522-40) to TGF β 1 and/or β 2 can be used to counter the adverse effects of TGF β 1, such as (i) promotion of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis, arterial injury, proliferative retinopathy, retinal detachment, myocardial infarction, post-angioplasty restenosis, scleroderma, vascular disorders, cataract, glaucoma, or esp. neural scarring and glomerulonephritis, also (not claimed) osteoporosis), or (ii) immune and inflammatory diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases or macrophage pathogen infection). Nucleic acids encoding human antibody VH and VL can be used for production of recombinant antigen-binding domains. These are highly specific, have low dissociation constants (pref. less than 5 nM) and low IC50s for neutralisation.

	Query Match	72.5%	Score	668:	DB	23:	Length	123:
	Best Local Similarity	73.6%	pred	No	7	07e-44:		
	Matches	92:	Conservative	15:	Mismatches	16:	Indels	2:
bb	1	qqlvsggqvqpors	rlscaasgfttssyqmhvwrqpqkalewvavsydsakyy	60				
yy	1	EVVLLEGGGVGF	QKSLRLSCAASGFTFKTCMHVWPQADGKCLFWVACISFWGSGNOYY	60				
bb	61	adsvkrftisrdns	knltlylqmnslraedtavvyccartge-ysgydtsc-vellwaqgtt	118				
yy	61	ADSVKGRFIVSR	DNSRDTVFLQMSLRLEDIAVYVCATGSPFGSIKRYLYLFWNWQGTI	120				
bb	119	vtvss	123					
yy	121	vtvss	125					

RESULT 8
 R22571 standard; protein: 115 AA.
 AC R22571:
 DT 21-MAY-1992 (first entry)
 DE Heavy chain VH3.5 from BSA binding scFv fragment.
 FE Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
 FL plus; gfp; binding; adsorption; gene VII; diverse repertoire;
 KW specific binding pairs; replicable genetic display package; human.
 OS Homo sapiens.
 PN W09201047-A.
 PP 23-JAN-1992.
 PP 10-JUL-1991: G01134.
 PP 10-JUL-1990: GB-015198.
 PP 19-OCT-1990: GB-022845.
 PP 12-NOV-1990: GB-024503.
 PP 06-MAR-1991: GB-004744.
 PP 15-MAY-1991: GB-010549.
 PP (CMB-) CAMBRIDGE ANTIBODY.
 PA (MEDI-) MED PES COUNCIL.
 PI McCafferty J, Pope AR, Johnson KS, Hoozeboom HRJ, Griffiths AD;
 PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
 PI Winter GP, Bonnett TP;
 PI WPL: 92-056862/07.
 PR Producing members of specific binding pairs - by expression in
 PT recombinant host cells with a secreting replicable genetic
 PT display package.
 PT Table 11: Page 152: 109pp: English.
 PS PCR was used to prepare a human scFv library from RNA from white
 PS blood cells from an immunised donor. Heavy chains from IgG and
 PS IgM antibodies were amplified separately. Four separate libraries
 PS were generated (IgG-K, IgG-lambda, IgM-K and IgM-lambda). The
 PS purified scFv fragments were ligated into the phagemid pHEM1 for
 PS expression on the surface of fd bacteriophage as gene III fusions.
 PS The clones were then subjected to affinity selection for binding
 PS to phox:BSA by selection on tubes followed by analysis by ELISA. of

(USSH) US DEPT HEALTH & HUMAN SERVICES.
A Benhar I, Brinkmann U, Fitzgerald D, Jung S, Lee B:
I Padlan EA, Pai L, Pastan I, Willingham M:
R WPI. 96:251462/25.
R Single chain fusion proteins and antibodies - useful to diagnose and
T treat cancer, specifically bind Lewis(X) related carbohydrate
T antigen
T Example 13: Figure 11A: 116pp: English.
S A novel recombinant DNA molecule which encodes a single chain fusion
S protein or antibody comprising the Fv region of both the light and
C heavy chains of an antibody (Ab) fused together, and an effector
C molecule, where the fusion protein or Ab has the binding specificity
C of monoclonal Ab (MAB) B1, B3 or B5, can be used for the production
C of such fusion proteins or antibodies. The fusion proteins can be
C used in compositions as an immunotoxin to inhibit tumour cell growth
C The single chain antibody can be used to detect the presence or
C absence of cells bearing a Lewis(X) carbohydrate antigen in a
C patient. The antibodies are also useful as multiple targeting
C moieties, providing at least 2 kinds of biological activity. They
C can also be used in diagnostic assays and for the imaging of tumours
C when attached to a radiolabel and for the pathological diagnosis of
C tumours. Humanised antibodies are less immunogenic than the mouse
C Mabs B1, B3 and B5, making them more suitable for long term
C treatment.
C Sequence. 119 AA:
C
C

Query Match	72.68:	Score 669,	DB 18:	Length 119:
Best Local Similarity	75.28:	Pred. No. 5.86e-44:		
Matches	94:	Conservative	16:	Mismatches 9; Indels 6; Gaps
Ddb	1	qvelvesggvvpgrslrliscaasftfssvamhwrgapkgjlewavvisydsnkyy	60	
Qoy	1	EVQLLESGGVVQGRSLRLSCAASGFTFKTYGMHWVRQAPGKLEWVAGISFDGSNQYY	60	
Ddb	61	adsvkgrftisrdskntlylqmnsiraedtavvyccarr-s---a-rt-vyfdwaggatl	119	
Qoy	61	ADSVKGRFIVSRDNRSDTVFLQWSLSRLIEDTAVYVCATECGSPFGSIKRGYLEWNMGOGTL	120	
Ddb	115	vfvass	119	
Qy	121	VTVSS	125	

RESULT	7	
ID	W15535 standard. Protein; 123 AA.	
AC	W15535;	
AD	27-NOV-1997 (first entry)	
DE	Anti-TGF beta-1 scfv antibody 31C9 VH domain.	
DE	Transforming growth factor beta-1; TGF-beta-1; human;	
DE	antibody engineering; scFv; phage display; lung fibrosis;	
KW	arterial injury; proliferative retinopathy; retinal detachment;	
KW	adult respiratory distress syndrome; liver cirrhosis;	
KW	post myocardial infarction; post-angioplasty restenosis;	
KW	scleroderma; vascular disease; cataract; glaucoma; scarring;	
KW	glomerulonephritis; osteoporosis; immune disease; inflammation;	
KW	rheumatoid arthritis; macrophage deficiency disease;	
KW	macrophage pathogen infection; therapy.	
KW	Homo sapiens.	
PN	GB2305921-A.	
PD	23-APR-1997	
PF	07-OCT-1996; 020920.	
PR	19-JAN-1996; GB-001081.	
PR	06-OCT-1995; GB-020486.	
PR	(CAMEB-) CAMBRIDGE ANTIBODY TECHNOLOGY.	
PI	Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;	
PI	Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;	
PI	Wilton AJ;	
PI	WPI: 97-215360/20.	
DR	N-PSDB; T60381.	
DR	Agent conts. antigen-binding domain of human antibody to	
PT	transforming growth factor beta 1 or 2 - and nucleic acid encoding	
PT	it, used to neutralise effects of TGF, e.g. for control of fibrosis,	
PT	immune and inflammatory disease	
PT		

CC 96 clones analysed, 43 showed binding to both phox:BSA and BSA.
 CC These were designated BSA binders. Thirteen of fourteen clones
 CC sequenced had the same sequence, the VH derived from a human VH3
 CC family gene (shown here) and the VL from a human V lambda 3 family
 CC gene (R2572). The other was derived from a human VH4 family gene
 CC and a human VK1 family gene. One clone bound only to phox:BSA
 CC (oxazolone binder). This sequence revealed a VH derived from a
 CC human VH1 family gene (R22569) and VL from a human V lambda 1
 CC family gene (R25707).
 CC See also F21260-307, 309-312, F23450, F22565, F23567-81
 SQ Sequence 115 AA;

Query Match 72.3%; Score 666; DB 4; Length 115;
 Best Local Similarity 75.6%; Pred. No. 1.03e-43;
 Matches 90; Conservative 15; Mismatches 10; Indels 4; Gaps 3;

Db 1 qvldsggrrvqgrrslrlscaasgffsfssygmhwrvgapqgklowvavlsydgskyy 60
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 QY 1 EVQLLESGGVVQPGRRSLRLSCLSAASGFTFKYGMHWRVQAPGKGLWVAGISFDGSGNOYY 60

Db 61 adsvkgrfivsrndskntlylqmslrdaedvayyycaktg--yysggwgyf-dywgqgt 115
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 QY 61 ADVSKGRFIVSRNSDPTVFLQMSLSRLPLEDTAVYYCATEGSPFGSIKGRVYLENWSGIL 119

RESULT 9

ID R52064 standard; Protein, 120 AA.
 AC R52064;

DT 11-OCT-1996 (first entry)
 DE Heavy chain variable region of human G36005 antibody.
 KW antibody; humanised; murine; human; heavy chain; light; variable;
 KW framework region; complementarity determining region; reshaping;
 KW modelling; surface residue; modify.
 OS Homo sapiens. Location/Qualifiers
 FH Key 1 30
 FT Region 1 30
 FT /label= framework_region_1
 FT /note= "FR 1"
 FT Region 31..35
 FT /label= complementarity_determining_region_1
 FT /note= "CDR 1"
 FT Region 36..49
 FT /note= "FR 2"
 FT Region 50..59
 FT /note= "CDR 2"
 FT Region 60..98
 FT /note= "FR 3"
 FT Region 99..110
 FT /note= "CDR 3"
 PN EP-592106-A1.
 PD 13-APR-1994.
 PF 07-SEP-1993; 307051.
 PR 09-SEP-1992; US-942245.
 PA (PEDE/) PEDERSEN JT.
 PA (IMMUG-) IMMUNOGEN INC.
 PI Guild BC, Pedersen JT, Pees AP, Poguska MA, Searle SMJ.
 WP1: 94-12030715.
 DR Method of resurfacing of rodent antibodies to produce humanised
 PT antibody forms - for producing non-human antibodies with improved
 PT therapeutic efficiency by presenting human surface on V-region
 PS Example 1, Fig 4B, 230pp; English.
 CC Modification of a rodent antibody (Ab) or fragment by resurfacing in
 CC order to produce a humanised rodent Ab can be determined by calculating
 CC homology between murine and human Ab antibody surfaces. In order to test
 CC the resurfacing approach of the invention, three humanisation experiments
 CC were set up: (1) traditional loop grafting; (2) resurfacing approach
 CC using most similar chain; and (3) resurfacing approach using human
 CC sequences with most similar surface residues. The Ab used was the murine
 CC anti-N901 Ab (see R52064). Experiment 2 was carried out using the present
 CC sequence which represents the human G36005 Ab heavy chain variable region
 CC with 89 percent homology with anti-N901 Ab N901/536005 (P52065) was
 CC prepd. by CDR grafting. Sequence numbering starts at 114 in the
 CC specification.

SQ Sequence 120 AA;

Query Match 72.3%; Score 666; DB 17; Length 120;
 Best Local Similarity 74.2%; Pred. No. 1.03e-43;
 Matches 92; Conservative 15; Mismatches 13; Indels 4; Gaps 3;

Db 1 qvldsggrrvqgrrslrlscaasgffsfssygmhwrvgapqgklowvavlsydgskyy 60
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 QY 1 EVQLLESGGVVQPGRRSLRLSCLSAASGFTFKYGMHWRVQAPGKGLWVAGISFDGSGNOYY 60

Db 61 adsvkgrfivsrndskntlylqmslrdaedvayyycaktg--a-lf-dywgqgt 116
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
 QY 61 AFSVKGPFIVSRNSDPTVFLQMSLSRLPLEDTAVYYCATEGSPFGSIKGRVYLENWSGIL 120

Db 117 vtvs 120
 :||||:
 QY 121 vtvs 124

RESULT 10

ID W01522 standard; Protein, 141 AA.
 AC W01522;

DT 03-MAR-1997 (first entry)
 DE Monoclonal antibody p61-1 heavy chain variable region.
 KW Monoclonal antibody; diagnosis; treatment; infection; hepatitis B;
 KW xenogeneic hybridoma; SPAZ 4; p61-1; ZM1-1; ZM1-2; MD3-4; L03-3;
 KW IgG1 class; heavy chain; light chain; variable region.
 OS Homo sapiens. Location/Qualifiers
 FH Key 1 119
 FT Peptide 1..19
 FT /label= leader_sequence
 FT Region 20..117
 FT /label= V_H(III) region
 FT Region 20..49
 FT /label= framework_region_1
 FT /note= "FR1"
 FT Region 50..53
 FT /label= complementarity_determining_region_1
 FT /note= "CDR1"
 FT Region 54..69
 FT /label= FR2
 FT Region 70..85
 FT /label= CDR2
 FT Region 86
 FT /label= FR3
 FT /note= "start of FR3 region"
 FT Region 118..129
 FT /label= D_segment
 FT Region 130..141
 FT /label= J_H4_region
 PN US5565354-A.
 PD 15-OCT-1996.
 PF 05-SEP-1986; 904517.
 PR 05-SEP-1986; US-904517.
 PR 31-OCT-1986; US-925196.
 PR 11-MAY-1988; US-192754.
 PR 15-JUN-1990; US-538796.
 PR 27-MAR-1991; US-676036.
 PR 21-APR-1992; US-871426.
 PR 14-JUN-1994; US-259372.
 PA (SANO) SANGUOZ LTD.
 PI Ostberg LG;
 DR WP1: 96-476304/47.
 DR N-PSDB: T46128.
 DR Human monoclonal antibodies specific for hepatitis B surface antigen
 PT are used to treat or prevent infection or in diagnostic assays
 PS Claim 4; Colman 27:28; 26pp; English.
 CC Monoclonal antibodies effective for the diagnosis and treatment of
 CC diseases caused by infection with hepatitis B have been prepared from a
 CC cell line obtained by fusing a xenogeneic hybridoma designated SPAZ 4
 CC with blood cells of a patient immunised with hepatitis B vaccine.
 CC Specific antibodies are p61-1, ZM1-1, ZM1-2, MD3-4 and L03-3, each of
 CC these being of the IgG1 class. The present sequence is the heavy

CC tumor cell line can be improved by genetic modifications.
SQ Sequence 140 AA;

Query Match 70.9%; Score 653; DB 23; Length 140;
Best Local Similarity 69.6%; Pred. No. 1,18e-42;
Matches 87; Conservative 20; Mismatches 17; Indels 1; Gaps 1;
Db 1 gqqlvsggqglvqpqgsrlrscasgffsfssyanswrdapqkalewvaaisggstyy 60
QY 1 EVQLLESGGGVQVQPSIPLSCAASGFTFKYGMHWVPQAPGKLEWVAGISFDGSGNY 60
Db 61 adsvkgrftrdsnkntllgmnlraedatavvycaar-gwqlrgeegdyvmdwvkgktm 119
QY 61 ADSVKGRFIVSRNSRDIVFLQMSLRLEDAVYVYCATGSGFSGIKRYYLEWVGSGTL 120
Db 120 vtvs 124
QY 121 VTVSS 125

RESULT 13
ID R54047 standard; Protein, 143 AA.
AC R54047;
DE 08-NOV-1994 (first entry)
KW Sequence of the VH region of monoclonal antibody PE1-1 against
DE Hepatitis B virus surface antigen.
KW Hepatitis B virus; surface antigen; monoclonal antibody; therapy;
KW HBsAg; diagnosis; HBV.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= leader
FT /label= leader
FT /label= VH III
FT /label= VH III
FT /label= CDR 1
FT /label= CDR 2
FT /label= D
FT /label= JH 4
FT /label= JH 4
PN WO9411495-A.
PD 26-MAY-1994.
PF 06-NOV-1992; U09749.
PR 06-NOV-1992; WO-009749.
PA (SANO) SANDOZ LTD.
PI Ostberg LG; 22.
DR N-PSDB; Q64050.
PT Monoclonal antibodies active against Hepatitis B surface antigen
PT - for diagnosis and treatment of Hepatitis B virus
PS Example; Page 35, 53pp; English.
CC Human volunteers were immunised with hepatitis B vaccine. MD3-4, ZM1-
CC 2, ZM1-1 and PE1-1 hybridoma cell lines were derived from
CC lymphocytes of individuals immunised with Heptavax (Merck & Co).
CC Antibodies PE1-1, ZM1-1, ZM1-2 and MD3-4 belong to the IgG1 class.
CC The cell lines producing PE1-1, ZM1-1 and ZM1-2 were deposited as
CC ATCC HB9234, 9191 and 9192 respectively. The cell lines all behave
CC as typical (mouse x human) x human hybridomas and produce their
CC respective Abs in concs. ranging up to 25 mg/l in standard
CC suspension culture. The heavy variable (VH) and light variable (LH)
CC chains of Abs PE1-1, ZM1-1, ZM1-2 and MD3-4 were isolated and
CC sequenced. Total RNA was extracted from 10(7) hybridoma cells
CC of each cell line. ss DNA was synthesised using AMV-reverse
CC transcriptase and oligo-dT as primer. PCRs were performed and
CC amplified DNA was size selected. ss DNA for sequencing was isolated
CC from each positive clone after superinfection with M13K07.
CC Sequencing was by the dideoxy chain termination method (Sanger
CC et al.).
SQ Sequence 143 AA;

Query Match 70.7%; Score 651; DB 9; Length 143;

Best Local Similarity 74.2%; Pred. No. 1,20e-42;
Matches 92; Conservative 10; Mismatches 19; Indels 3; Gaps 1;
Db 20 gqqlvsggqglvqpqgsrlrscasgffsfssyanswrdapqkalewvaaisggstyy 79
QY 1 EVQLLESGGGVQVQPSIPLSCAASGFTFKYGMHWVPQAPGKLEWVAGISFDGSGNY 60
Db 80 adsvkgrftrdsnkntllgmnlraedatavvycaadgylfasgspghy---wvqgtl 136
QY 61 ADSVKGRFIVSRNSRDIVFLQMSLRLEDAVYVYCATGSGFSGIKRYYLEWVGSGTL 120
Db 137 vtvt 140
QY 121 VTVS 124
RESULT 14
ID R54788 standard; peptide; 125 AA.
AC R54788;
DE 18-OCT-1994 (first entry)
DE SPA-reactive IgM heavy chain clone KIM
KW SPA domain D; Ig binding region; IgM; B-cell superantigen; sAg,
KW superantigen; heavy chain variable region; VH3 restricted antibody;
KW VH; protein-A; KIM; B-lymphocyte; vaccine.
OS Homo sapiens.
PN WO9409818-A.
PD 11-MAY-1994.
PF 29-OCT-1993; U10555.
PR 30-OCT-1992; US-969936.
PA (REGC) UNIV CALIFORNIA.
PI Silverman GJ;
DR WPI; 94-167127/20.
PT Stimulating prodn. of variable region gene family restricted
PT antibodies - through B-cell super-antigen vaccination
PS Disclosure; Page 70; 130pp; English.
CC A B-cell superantigen (sAg) is a fragment of SpA D domain that
CC specifically binds the Fab portion of variable region of VH, especially
CC VH3, restricted Abs. During attempts to identify sAg's, aa sequences
CC (R54784-801) of H chains from Ig reactive with mod-SPA, and aa and
CC DNA sequences (R54802-16, Q64842-56) of VH regions of SpA binders
CC obtained from combinatorial libraries were determined. IgM protein
CC KIM is derived from the germline configuration of a VH gene
CC segment.
SQ Sequence 125 AA;

Query Match 70.6%; Score 650; DB 9; Length 125;
Best Local Similarity 68.8%; Pred. No. 2,07e-42;
Matches 80; Conservative 20; Mismatches 19; Indels 0; Gaps 0;
Db 1 gqqlvsggqglvqpqgsrlrscasgffsfssyanswrdapqkalewvaaisggstyy 60
QY 1 EVQLLESGGGVQVQPSIPLSCAASGFTFKYGMHWVPQAPGKLEWVAGISFDGSGNY 60
Db 61 vdsr-kgrftrdsnkntllgmnlraedatavvycaaklstaasgfftdymdwqgttl 120
QY 61 ADSVKGRFIVSRNSRDIVFLQMSLRLEDAVYVYCATGSGFSGIKRYYLEWVGSGTL 120
Db 121 vtvs 125
QY 121 VTVSS 125
RESULT 15
ID R54789 standard; peptide; 125 AA.
AC R54789;
DE 18-OCT-1994 (first entry)
DE SPA-reactive IgM heavy chain clone RIV.
KW SPA domain D; Ig binding region; IgM; B-cell superantigen; sAg;
KW superantigen; heavy chain variable region; VH3 restricted antibody;
KW VH; protein-A; RIV; B-lymphocyte; vaccine.
OS Homo sapiens.
PN WO9409818-A.

US-08-844-215-4.rag

Thu Feb 26 07:05:59 1998

PD 11-MAY-1994.
 PF 29-OCT-1993: U10555.
 PR 30-OCT-1992: US-969936.
 PA (REGC) UNIV CALIFORNIA.
 PI Silverman GJ:
 DR WPI. 94-167127/20.
 PT Stimulating prodn. of variable region gene family restricted
 PT antibodies - through B-cell super-antigen vaccination
 PS Disclosure; Page 71: 130pp; English.
 CC A B-cell superantigen (sAg) is a fragment of SpA D domain that
 CC specifically binds the Fab portion of variable region of VH, especially
 CC antibodies. The sAg is used to enhance production of VH, especially
 CC VH3, restricted Abs. During attempts to identify sAgs, aa sequences
 CC (R54784-801) of H chains from Ig reactive with mod-SpA, and aa and
 CC DNA sequences (R54802-16, 064842-56) of VH regions of SpA binders
 CC obtained from combinatorial libraries were determined. IgM protein
 CC RIV is derived from the germline configuration of a VH gene
 CC segment.
 SQ Sequence 125 AA:

Query Match 70.6%; Score 650; DB 9; Length 125;
 Best Local Similarity 68.8%; Pred. No. 2,07e-42;
 Matches 86; Conservative 20; Mismatches 19; Indels 0; Gaps 0:

Db	1	evqlvesgggvgvqgsrlrlscaasgftfssfamhwrqapkglewavmsysgdnkyy	60
QY	1	EVQLLESGGGVDPGRSLRLSCAASGFTFTKTYGMHWYRQAPKGLEWVAGISFDGSNOYY	60
Db	61	vdsvkqftisrdnskntlylqmnslraedtalycaklstaasgftfdtygmdwgqttl	120
QY	61	ADSVKGRFIVSRDNRSDTVFLQWSSLELEDTAVYYCATEGSPFGSIKGRYILENWCQCTL	120
Db	121	vtvss	125
QY	121	VTVSS	125

Search completed: Tue Feb 24 07:10:46 1998
 Job time : 35 secs.

W P S R E L A
***** (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:06:43 1998, MaxPar time 5 41 Seconds
Tabular output not generated. 501.596 Million cell updates/sec

Title: >US-08-844-215-3
Description: (1-128) from US08844215.pep
Perfect Score: 915
Sequence: 1 EVQLLEQSGAEVKKPGSSVK.....NCYPGFPOGWGQGLTVSS 128

Scoring table: PAM 150
Gap 11

Searched: 59021 seqs, 21210389 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34

1:part1 2:part2 3:part3 4:part4 5:parts 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 40.96%, Variance 67.604, scale 0.606

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	553	60.4	117	5	HV1A_HUMAN IG HEAVY CHAIN V-I RE	7.61e-105
2	484	52.9	117	5	HV1B_HUMAN IG HEAVY CHAIN PRECUR	4.63e-88
3	479	52.3	117	5	HV1G_HUMAN IG HEAVY CHAIN PRECUR	7.46e-87
4	470	51.4	143	5	HV1C_HUMAN IG HEAVY CHAIN PRECUR	1.12e-84
5	435	47.5	114	5	HV00_MOUSE IG HEAVY CHAIN V REGI	2.89e-76
6	431	47.1	125	5	HV1F_HUMAN IG HEAVY CHAIN V-I RE	2.52e-75
7	428	46.8	140	5	HV02_MOUSE IG HEAVY CHAIN PRECUR	1.37e-74
8	426	46.6	120	5	HV03_MOUSE IG HEAVY CHAIN V REGI	4.11e-73
9	424	46.3	124	5	HV1D_HUMAN IG HEAVY CHAIN V-I RE	1.24e-73
10	423	46.2	124	5	HV1E_HUMAN IG HEAVY CHAIN V-I RE	2.14e-73
11	414	45.2	122	5	HV3G_HUMAN IG HEAVY CHAIN V-I RE	3.01e-71
12	402	43.9	117	5	HV14_MOUSE IG HEAVY CHAIN PRECUR	2.16e-68
13	400	43.7	117	5	HV13_MOUSE IG HEAVY CHAIN V REGI	6.43e-68
14	400	43.7	117	5	HV12_MOUSE IG HEAVY CHAIN V REGI	6.43e-68
15	395	43.2	118	5	HV51_MOUSE IG HEAVY CHAIN V REGI	9.87e-67
16	394	43.1	117	5	HV52_MOUSE IG HEAVY CHAIN PRECUR	1.70e-66
17	391	42.7	117	5	HV05_MOUSE IG HEAVY CHAIN PRECUR	8.75e-66
18	389	42.5	117	5	HV04_MOUSE IG HEAVY CHAIN PRECUR	2.60e-65
19	389	42.5	117	5	HV05_MOUSE IG HEAVY CHAIN PRECUR	2.60e-65
20	389	42.5	120	5	HV50_MOUSE IG HEAVY CHAIN V REGI	2.60e-65
21	389	42.5	138	5	HV48_MOUSE IG HEAVY CHAIN PRECUR	2.60e-65
22	389	42.5	139	5	HV07_MOUSE IG HEAVY CHAIN PRECUR	2.60e-65

23	388	42.4	121	5	HV01_MOUSE IG HEAVY CHAIN V REGI	4.49e-65
24	388	42.4	126	5	HV3K_HUMAN IG HEAVY CHAIN V-I RE	4.49e-65
25	379	41.4	117	5	HV49_MOUSE IG HEAVY CHAIN PRECUR	6.01e-63
26	375	41.0	117	5	HV09_MOUSE IG HEAVY CHAIN PRECUR	5.24e-62
27	373	40.9	120	5	HV11_MOUSE IG HEAVY CHAIN PRECUR	1.56e-61
28	372	40.7	120	5	HV1R_HUMAN IG HEAVY CHAIN V-I RE	2.69e-61
29	371	40.5	121	5	HV3J_HUMAN IG HEAVY CHAIN V-I RE	4.62e-61
30	371	40.5	122	5	HV3H_HUMAN IG HEAVY CHAIN V-I RE	4.62e-61
31	365	39.9	117	5	HV10_MOUSE IG HEAVY CHAIN PRECUR	1.19e-59
32	363	39.7	119	5	HV3L_HUMAN IG HEAVY CHAIN V-I RE	3.51e-59
33	363	39.7	119	5	HV3N_HUMAN IG HEAVY CHAIN V-I RE	3.51e-59
34	360	39.3	117	5	HV3C_HUMAN IG HEAVY CHAIN PRECUR	1.78e-58
35	358	39.1	117	5	HV15_MOUSE IG HEAVY CHAIN PRECUR	5.23e-58
36	354	38.7	119	5	HV3M_HUMAN IG HEAVY CHAIN V-I RE	4.53e-57
37	354	38.7	120	5	HV3E_HUMAN IG HEAVY CHAIN V-I RE	4.53e-57
38	349	38.1	115	5	HV3F_HUMAN IG HEAVY CHAIN V-I RE	6.89e-56
39	347	37.9	115	5	HV3D_HUMAN IG HEAVY CHAIN V-I RE	1.96e-55
40	344	37.6	117	5	HV01_CATIG IG HEAVY CHAIN PRECUR	9.83e-55
41	343	37.5	117	5	HV02_CANFA IG HEAVY CHAIN V REGI	1.68e-54
42	341	37.3	117	5	HV3L_CAFAT IG HEAVY CHAIN PRECUR	4.92e-54
43	339	37.0	122	5	HV3A_HUMAN IG HEAVY CHAIN V-I RE	1.44e-53
44	335	36.6	144	5	HV26_MOUSE IG HEAVY CHAIN PRECUR	1.23e-52
45	334	36.5	114	5	HV3B_HUMAN IG HEAVY CHAIN V-I RE	2.09e-52

ALIGNMENTS

RESULT 1
ID HV1A_HUMAN STANDARD: PRT: 117 AA.
AC P01742;
DI 21-JUL-1986 (REL. 01, CREATED)
DI 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DI 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-I REGION (EU).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
PN [1]
PP SEQUENCE
RX MEDLINE: 71064024.
KA LUNNINGHAM B A, PUTISHAUSEP H, GALL W E, GOTTILIER P D.,
FA WAXDAL M J, EDELMAN G M;
PL RTOCHEMISTRY 9:3161-3170(1970).
RN [2]
RX MEDLINE: 71064027.
RX DISULFIDE BOND.
RA GALL W E, EDELMAN G M;
RL BIOCHEMISTRY 9:3188-3196(1970).
CC -1- THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
CC PIP: A02023; GHHEU.
DP HSSP: P01810; LEVB.
KW IMMUNOGLOBULIN V REGION.
FT MOD_PES 1
FT DISULFID 22 96
FT NONTER 117 117
SQ SEQUENCE 117 AA: FC99E17D CRO32;

Query Match 60.4%, Score 553, DB 5, Length 117,
Best local Similarity 80.6%, Pred No: 7.61e-105,
Matches 79, Conservative 10, Mismatches 8, Indels 1, Gaps 1;

Db 1 qvqlv-gsdaevkpkpssvkvskasggtfssailwrgpqqglomgqdivgmfgppp 59
|||||
QY 1 EVALLLEQSGAEVKKPGSSVKSGGGTFFSHVISWVQAPGCGGLEWVGSGISPFISN 60
60 yadkfagrtitadestntaymclslrscdtafyca 97
|||||
QY 61 SAQKFGVRSITADEASTAYMELSLRSEDTAIYYCA 98

RESULT 2
ID HV1B_HUMAN STANDARD: PRT: 117 AA.

Thu Feb 26 07:05:58 1998

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AC P01743; 1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-I REGION (HG3).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 83144028.
RA RECHAVI G., RAM D., GLAZER L., ZAKUT P., GIVOL D.:
RL PROC. NATL. ACAD. SCI. U.S.A. 80:855-859(1983).
DR EMBL; J00240; G553411.
DR PIR; A02024; HVH0HG.
DR HSP; P01810; LFVB.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (HG3).
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12946 MW; BCC8B1DB CRC32;

Query Match 52.9%; Score 484; DB 5; Length 117;
Best Local Similarity 70.7%; Pred. No. 4.63e-88;
Matches 70; Conservative 15; Mismatches 13; Indels 1; Gaps 1;

Db 20 qvqlv-qsgaevkpgasvksckasgytftgymhwvrgapggglewmglnpnsqgts 78
QY 1 EVOLLEQSGAEVKPKGSSVKVSKASGGTFSGHVSWVROAPGOGLEWMMGSGISFFCTSN 60

Db 79 yaqkfgrvtrtdstsvymelsrlsdsctavyycaar 117
QY 61 SAQKFGGRVSIITADESASTAYMELSLRSEDRTAIYYCAK 99

RESULT 3 STANDARD: PRT: 117 AA.
ID HV1G_HUMAN
AC P23083;
DT 01-NOV-1991 (REL. 20, CREATED)
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-I REGION (V35).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 88296408.
RA MATSUDA F., LEE K.H., NAKAI S., SATO T., KODAIRA M., ZONG S.Q.,
RA OHNO H., FUKUHARA S., HONJO T.:
RL EMBO J. 7:1047-1051(1988).
DR EMBL; X07448; -. NOT_ANNOTATED_CDS.
DR PIR; S00476; HVH035.
DR HSP; P01810; LFVB.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (V35).
FT NON_TER 117 117
FT SEQUENCE 117 AA; 13009 MW; FAA560D1 CRC32.

Query Match 52.3%; Score 479; DB 5; Length 117;
Best Local Similarity 70.7%; Pred. No. 7.49e-87;
Matches 70; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

Db 20 qvqlv-qsgaevkpgasvksckasgytftgymhwvrgapggglewmglnpnsqgts 78
QY 1 EVOLLEQSGAEVKPKGSSVKVSKASGGTFSGHVSWVROAPGOGLEWMMGSGISFFCTSN 60

Db 79 yaqkfgrvtrtdstsvymelsrlsdsctavyycaar 117
QY 64 SAQKFGGRVSIITADESASTAYMELSLRSEDRTAIYYCAK 99

RESULT 4 STANDARD: PRT: 143 AA.
ID HV1C_HUMAN
AC P01744; 1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-I REGION (ND) (FRAGMENTS).
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 83055234.
RA KENTEN J.H., MORGAN H.V., HOUGHTON M., DERRBYSHIRE R.B., VINEY J.:
RL P.L.O., GOUJID H.J.:
FL P.L.O., NATL. ACAD. SCI. U.S.A. 79:6661-6665(1982).
RN [2]
RN SEQUENCE OF 16-142.
RA BENNIC H.H., JOHANSSON S.G.O., VON BAHR-LINDSTROM H.:
RL (IN) IMMEDIATE HYPERSENSITIVITY: MODERN CONCEPTS AND DEVELOPMENTS,
RL BACH M.K., ED., PP.1-36, MARCEL DEKKER, NEW YORK, (1978).
CC -1- THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A02026; EIHUND.
DR HSP; P01607; LFVB.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT NON_CONS 4 5
FT SIGNAL 1 15
FT CHAIN 16 143 IG HEAVY CHAIN V REGION (ND).
FT MOD_RES 16 16 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 37 111
FT CONFLICT 17 17 T -> V (IN REF. 2).
FT CONFLICT 49 50 IH -> HI (IN REF. 2).
FT CONFLICT 63 64 VG -> GV (IN REF. 2).
FT CONFLICT 121 121 MISSING (IN REF. 2).
FT NON_TER 143 143
FT SEQUENCE 143 AA; 16051 MW; 6D605E13 CRC32;

Query Match 51.4%; Score 470; DB 5; Length 143;
Best Local Similarity 56.9%; Pred. No. 1.12e-84;
Matches 74; Conservative 23; Mismatches 29; Indels 4; Gaps 4;

Db 16 qqlv-qsgaevkpgasvksckasgytftgymhwvrgapggglewmglnpnsqgts 74
QY 1 EVOLLEQSGAEVKPKGSSVKVSKASGGTFSGHVSWVROAPGOGLEWMMGSGISFFCTSN 60

Db 75 yaqkfgrvtrtdstsvymelsrlsdsctavyycaar 133
QY 61 SAQKFGGRVSIITADESASTAYMELSLRSEDRTAIYYCAKDPPTSGGNCYP-GF-PQOW 118

RESULT 5 STANDARD: PRT: 114 AA.
ID HVCO_MOUSE
AC P01741;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (ANTI-ARSONATE ANTIBODY).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RN SEQUENCE
RC STRAIN-A/J;
RX MEDLINE; 79195438.
RA CAPRA J.D., NISONOFF A.:
RL J. IMMUNOL. 123:279-284(1979).
CC -1- ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF THE IGG1
CC SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V REGION
CC SEQUENCE.

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DR PIR: A02022; GLMSAA.
 DR HSSP: P01772; 1PCV
 KW IMMUNOGLOBULIN V REGION: ANTIARSONATE ANTIBODY
 FT NON_TER 114
 SQ SEQUENCE 114 AA: 12555 MW: 1A027F1D CPC32.

Query Match 47.5%; Score 435; DB 5; Length 114;
 Best Local Similarity 67.0%; Pred. No. 2 89a-76;
 Matches 71; Conservative 19; Mismatches 12; Indels 4; Gaps 4.

Db 1 evql-qsgaelvkgssvskmsckatgytfssyelyvvrqapggldlg-yissssayp 58
 QY 1 EVQLLEQSGAEVKKPGSSVKVSKASGCTFSCHVISWVQAPGQGLEWMGGGISFFGT-S 59

59 nyackfqrvtitadestntaymelslrsdtaivcavrvsry 104

QY 60 NSAKFGQSPVSTADESASTAYMELSLPSEDTAIYVCA-KDPPFF 104

RESULT 6
 ID HVLF_HUMAN STANDARD: PRT: 125 AA
 AC P06326;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V-1 REGION (MOT).
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.

RX MEDLINE: 86203277.
 RA KOJIMA M., KOIDE T., ODANI S., ONO T.;
 RL MOL. IMMUNOL. 23:169-174(1986).

DR PIR: A02025; HVHMO
 DR HSSP: P01772; 8FAB
 KW IMMUNOGLOBULIN V REGION
 FT DOMAIN 1 98 V SEGMENT.
 FT DOMAIN 94 107 D SEGMENT
 FT DOMAIN 108 125 J SEGMENT
 FT DISULFID 22 96 HY SIMILARITY.
 FT NON_TER 125 125
 SQ SEQUENCE 125 AA: 13573 MW: 6745023 CPC32.

Query Match 47.1%; Score 431; DB 5; Length 125;
 Best Local Similarity 49.2%; Pred. No. 2 62a-75.
 Matches 63; Conservative 26; Mismatches 36; Indels 3; Gaps 3.

Db 1 qvqlv-qsgaelvkgssvskmsckatgytfssyelyvvrqapggldlg-yissssayp 59
 QY 1 EVQLLEQSGAEVKKPGSSVKVSKASGCTFSCHVISWVQAPGQGLEWMGGGISFFGT-S 60

60 ygrsqarftvtrdsstttvymetalisadtaivcarga-hysdtdsgtsl-gpwgg 117
 QY 61 SAAKFGQSPVSTADESASTAYMELSLPSEDTAIYVCAKDPKPCSGN:YPCFFQWQ 120

Db 118 gtlivss 125
 QY 121 GTLTVSS 128

RESULT 7
 ID HV02_MOUSE STANDARD: PRT: 140 AA.
 AC P01746;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (93G7).

OS MUS MUSCULUS (MOUSE).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-A/J;
 RX MEDLINE: 82152818.
 RA SIMS J., BARBITTS T.H., ESTESS P., SLAUGHTER C., TUCKER P.W.,
 PA CAPRA J.D.;
 PL SCIENCE 256:30a-311(1982);
 DR EMBL: J00493; G195007; -;
 DR PIR: A02028; HVMSG7.
 DR HSSP: P0178a; 6FAB
 KW IMMUNOGLOBULIN V REGION: ANTIARSONATE ANTIBODY. HYBRIDOMA. SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION (93G7).
 FT NON_TER 140 140
 SQ SEQUENCE 140 AA: 15514 MW: 070005C8 CPC32;

Query Match 46.8%; Score 428; DB 5; Length 140;
 Best Local Similarity 54.7%; Pred. No. 1 37a-74;
 Matches 70; Conservative 27; Mismatches 24; Indels 7; Gaps 6;

Db 20 evql-qsgaelvragssvskmsckatgytfssyginwtkqrpqgglewginpangvin 78
 QY 1 EVQLLEQSGAEVKKPGSSVKVSKASGCTFSCHVISWVQAPGQGLEWMGGGISFFGT-S 60

Db 79 yrekfkgtltvdkssstajmqlsltsodsavvfcar--shyy-ggs-y-df-dywgq 132
 QY 61 SACKFGQSPVSTADESASTAYMELSLPSEDTAIYVCAKDPKPCSGN:YPCFFQWQ 120

Db 133 gtlvtvss 140
 QY 121 GTLTVSS 128

RESULT 8
 ID HV03_MOUSE STANDARD: PRT: 120 AA
 AC P01747;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (36-65).
 OS MUS MUSCULUS (MOUSE).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE: 83131846.
 RA SIEKEVITZ M., GEETTER M.L., BRODIE P., PIRLET P.,
 RA MAPSHAK, POTSTEIN A.;
 PL Exp. J. IMMUNOL. 12:1023-1032(1982).
 CC - FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES
 CC THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF
 CC THESE V REGIONS HAVE REARRANGED TO THE SAME J SEGMENT, JH2.

DR PIR: A0204; HVMSG7
 DR HSSP: P01789; 6FAB.
 KW IMMUNOGLOBULIN V REGION: ANTIARSONATE ANTIBODY. HYBRIDOMA.
 FT NON_TER 120 120
 SQ SEQUENCE 120 AA: 13307 MW: BSAPOCAL CPC32;

Query Match 46.6%; Score 426; DB 5; Length 120;
 Best Local Similarity 53.5%; Pred. No. 4 11e-74;
 Matches 58; Conservative 20; Mismatches 23; Indels 7; Gaps 6;

Db 1 vql-qsgaelvragssvskmsckatgytfssyginwtkqrpqgglewginpangvin 59
 QY 2 VALLEQSGAEVKKPGSSVKVSKASGCTFSCHVISWVQAPGQGLEWMGGGISFFGT-S 61

Db 60 nekfkgtltvdkssstajmqlsltsodsavvfcar--shyy-ggs-y--fdywgq 113
 QY 62 AKKFGQSPVSTADESASTAYMELSLPSEDTAIYVCAKDPKPCSGN:YPCFFQWQ 121

Db 114 tltvss 120
 QY 122 TLTVSS 128

```

RESULT 9
ID HV14_HUMAN STANDARD PRT: 124 AA
AC P01760:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-I REGION (WOL).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046599.
RA ANDREWS D.W., CAPRA J.D.;
RL BIOCHEMISTRY 20:5822-5830(1981).
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A02043; M1HWL.
DR HSSP: P01607; IFGV.
KW IMMUNOGLOBULIN V REGION.
FT MOD_RES 1 1
FT NON_TER 124 124
FT SEQUENCE 124 AA: 13684 MW; 479BD3BE CRC32;
SQ
Query Match 46.3%; Score 424; DB 5; Length 124;
Best Local Similarity 55.8%; Pred. No. 1.24e-73; Indels 8; Gaps 7;
Matches 72; Conservative 20; Mismatches 29;
Db 1 qvqlm-qsgaevkpgssvrvscsksgtfdykgdwirgpgkgglewqgdlprfngv 59
QY 1 EVQLLEQSGAEVKKPGSSVKVKSGKSGTFSCHVISWVRQAPGQGLFWMGG-SISFGTS 59
Db 60 knpqs-vrvsvslkpsfnqahmelslfsedtavvycaeyg-f-dtsdyv---yy-wg 113
QY 60 NSAQKFGQVRISITADESASTAYMELSLRSEDATAYYCAKDPFRPCSGNGCYPGFVQWG 119
Db 114 qgtlvtvss 122
QY 120 QGTLVTVSS 128
RESULT 10
ID HV14_HUMAN STANDARD PRT: 124 AA.
AC P01761:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-I REGION (SIE).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 82046599.
RA ANDREWS D.W., CAPRA J.D.;
RL BIOCHEMISTRY 20:5822-5830(1981).
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
CC ACTIVITY.
DR PIR: A02044; M1HWI.
DR HSSP: P01857; 2FGW.
KW IMMUNOGLOBULIN V REGION.
FT MOD_RES 1 1
FT NON_TER 124 124
FT SEQUENCE 124 AA: 13732 MW; C1E9663D CRC32;
SQ
Query Match 46.2%; Score 423; DB 5; Length 124;
Best Local Similarity 54.3%; Pred. No. 2.14e-73;
Matches 70; Conservative 23; Mismatches 28; Indels 8; Gaps 6;
Db 1 qvqlv-qsgaevkpgssvrvrvtcktsqgtfsgytsiawrgagrgglewqgspakwtdpfq 59
QY 1 EVQLLEQSGAEVKKPGSSVKVKSGKSGTFSCHVISWVRQAPGQGLFWMGG-SISFGTSN 60

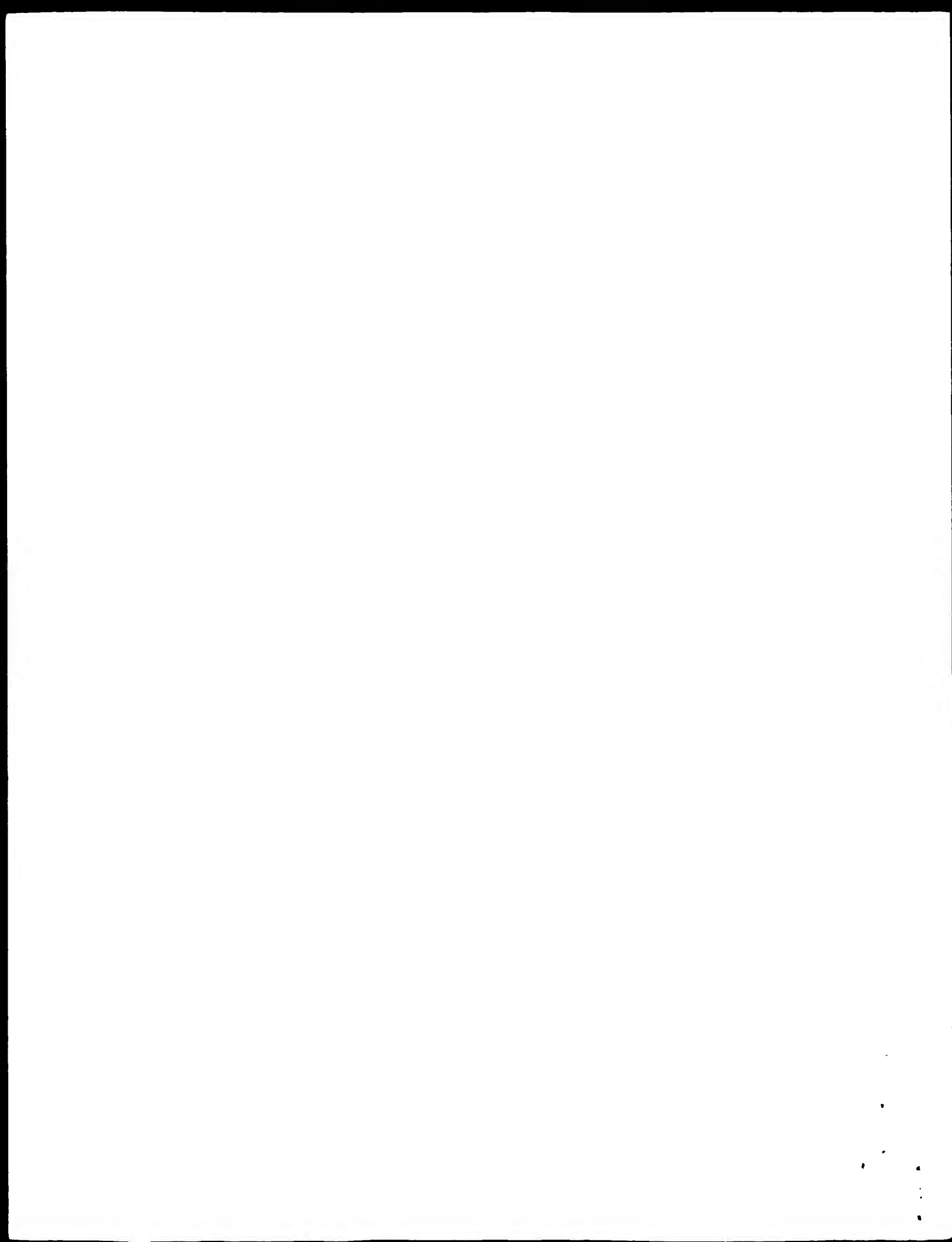
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Db 60 qvylkwe-rvltvsksfngaymclvnlfnedqavvycaew-k--qgvnvp---ldvwa 113
QY 61 SA-QKFGVGSIIADESASTAYMELSLRSEDATAYYCAKDPFRPCSGNGCYPGFVQWG 119
Db 114 qvylvtvss 122
QY 120 QGTLVTVSS 128
RESULT 11
ID HV36_HUMAN STANDARD PRT: 122 AA.
AC P01768:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (CAM).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 81013859.
RA LEHMAN D.W., PUTNAM F.W.;
RL PROC. NATL. ACAD. SCI U S A 77:3239-3243(1980).
CC -1- THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A PATIENT WITH
CC MACROGLOBULINEMIA.
DR PIR: A02051; M3HUAM.
DR HSSP: P01607; 2FGW.
KW IMMUNOGLOBULIN V REGION.
FT MOD_RES 1 1
FT NON_TER 122 122
FT SEQUENCE 122 AA: 12668 MW; 4AF3E3E6 CRC32;
SQ
Query Match 45.2%; Score 414; DB 5; Length 122;
Best Local Similarity 49.6%; Pred. No. 3.01e-71;
Matches 64; Conservative 30; Mismatches 27; Indels 8; Gaps 6;
Db 1 qvelve-sgggvvvparslriscasagfttsnyamhwrrgppkqlwva-vvisybblak 58
QY 1 EVQLLEQSGAEVKKPGSSVKVKSGKSGTFSCHVISWVRQAPGQGLFWMGG-SISFGTSN 60
Db 59 yvavskvkrftisrdbskbtlylqmmisraebtavvycaeyg-rp-qb yraf-nywa 119
QY 61 S-AQKFGQVRISITADESASTAYMELSLRSEDATAYYCAKDPFRPCSGNGCYPGFVQWG 119
Db 114 qgtlvtvss 122
QY 120 QGTLVTVSS 128
RESULT 12
ID HV14_MOUSE STANDARD PRT: 117 AA.
AC P01758:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (108A).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 81245215.
RA GIVOL D., ZAKUT R., EFFRON K., RECHAVI G., RAM D., COHEN J.R.;
RL NATURE 392:426-430(1981).
DR EMRL: J06488; G554028;
DR PIR: A02041; HVM58A.
DR HSSP: P01789; 1IGI.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117
FT NON_TER 117 117
FT SEQUENCE 117 AA: 12272 MW; 9412C0E1 CRC32;
SQ

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Search completed. Tue Feb 24 07:07:04 1998
Job time : 21 secs.




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RESULT 2
ENTRY
  Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)
  TITLE
  ORGANISM
  DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
  16-Aug-1996

ACCESSIONS
REFERENCE
  PH0952
  Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
  J. Exp. Med. (1992) 175:983-991
  #journal
  Evidence for somatic selection of natural autoantibodies.
  #cross-references MUID:92202880
  #accession
  PH0952
  #status
  nucleic acid sequence not shown
  #molecule_type DNA
  #residues
  1-129 ##label MAR
  #superfamily immunoglobulin V region; immunoglobulin homology
  heterotetramer; immunoglobulin
  #region framework 1\
  #domain immunoglobulin homology #label IMM\
  #region complementarity-determining 1\
  #region framework 2\
  #region complementarity-determining 2\
  #region framework 3\
  #region complementarity-determining 3
  #length 129 #molecular_weight 13932 #checksum 4075
  SUMMARY
  Query Match 69.6%; Score 637, DB 7, Length 129;
  Best Local Similarity 74.6%; Pred. No. 4,120-82;
  Matches 97; Conservative 14; Mismatches 16; Indels 4; Gaps 2;

CLASSIFICATION
KEYWORDS
  Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)
  #formal_name Homo sapiens #common_name man
  17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
  16-Aug-1996
  PH0952
  #type fragment
  #region framework 1\
  #domain immunoglobulin homology #label IMM\
  #region complementarity-determining 1\
  #region framework 2\
  #region complementarity-determining 2\
  #region framework 3\
  #region complementarity-determining 3
  #length 128 #checksum 3537
  SUMMARY
  Query Match 70.1%; Score 641, DB 7, Length 128;
  Best Local Similarity 73.6%; Pred. No. 9,160-83;
  Matches 95; Conservative 14; Mismatches 18; Indels 2; Gaps 2;

Db 1 qvqlv-qsgaevkpgssvkscasggtfssyaiswvrgapqgqlwmggipfqtan 59
  :|||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLEQSGAEVKKPGSSVKVKSCASGDTFSGHVISWVRQAPGQGLEWMGGSISFEGTSN 60
  :|||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 yaqkfgrvritadkststststststststststststststststststststst 119
  :|||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SAQKFGQSVISITADEASTAYMELSRSEDTAIYYCAKPPPPFSGGNGCYPCFQQWG 118
  :|||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 gqdtlvtvss 129
  :|||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 GQTLVTVSS 128

RESULT 4
ENTRY
  Ig heavy chain V region (G6+ CLL-AND) - human (fragment)
  TITLE
  ORGANISM
  DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
  16-Aug-1996
  PH0955
  #type fragment
  #region framework 1\
  #domain immunoglobulin homology #label IMM\
  #region complementarity-determining 1\
  #region framework 2\
  #region complementarity-determining 2\
  #region framework 3\
  #region complementarity-determining 3
  #length 127 #checksum 6297
  SUMMARY
  Query Match 69.4%; Score 635, DB 7, Length 127;
  Best Local Similarity 73.6%; Pred. No. 8,730-82;
  Matches 95; Conservative 15; Mismatches 16; Indels 4; Gaps 4;

CLASSIFICATION
KEYWORDS
  Ig heavy chain V region (G6+ CLL-AND) - human (fragment)
  #formal_name Homo sapiens #common_name man
  17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
  16-Aug-1996
  PH0955
  #type fragment
  #region framework 1\
  #domain immunoglobulin homology #label IMM\
  #region complementarity-determining 1\
  #region framework 2\
  #region complementarity-determining 2\
  #region framework 3\
  #region complementarity-determining 3
  #length 127 #checksum 6297
  SUMMARY
  Query Match 69.4%; Score 635, DB 7, Length 127;
  Best Local Similarity 73.6%; Pred. No. 8,730-82;
  Matches 95; Conservative 15; Mismatches 16; Indels 4; Gaps 4;

Db 1 qvqlv-qsgaevkpgssvkscasggtfssyaiswvrgapqgqlwmggipfqtan 59
  :|||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLEQSGAEVKKPGSSVKVKSCASGDTFSGHVISWVRQAPGQGLEWMGGSISFEGTSN 60
  :|||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 yaqkfgrvritadkststststststststststststststststststststst 118
  :|||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SAQKFGQSVISITADEASTAYMELSRSEDTAIYYCAKPPPPFSGGNGCYPCFQQWG 119
  :|||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 gqdtlvtvss 127
  :|||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 GQTLVTVSS 128

RESULT 3
ENTRY
  Ig heavy chain V-1 region (NEI) - human
  TITLE
  ORGANISM
  DATE 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
  16-Aug-1996
  A33548; PH0956
  Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.;
  Carson, D.A.
  Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
  #journal
  Developmentally restricted immunoglobulin heavy chain
  #title
  variable region gene expressed at high frequency in chronic
  lymphocytic leukemia.
  #cross-references MUID:89345575
  #accession
  A33548
  #status
  preliminary; not compared with conceptual translation
  #molecule_type mRNA
  #residues
  1-129 ##label KIP
  PH0952
  Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
  J. Exp. Med. (1992) 175:983-991
  #journal
  Evidence for somatic selection of natural autoantibodies.
  #cross-references MUID:92202880
  #accession
  PH0956
  #status
  nucleic acid sequence not shown
  #molecule_type DNA

```

```

RESULT      5
ENTRY       B33548
TITLE       #type complete
ORGANISM    Ig heavy chain V-1 region (AND) - human
DATE        #formal_name Homo sapiens #common_name man
            17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
            16-Aug-1996

ACCESSIONS  B33548
REFERENCE    Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.;
            Carson, D.A.
            Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5933-5937
            Developmentally restricted immunoglobulin heavy chain
            variable region gene expressed at high frequency in chronic
            lymphocytic leukemia.

#cross-references MUID:89345575
#accession      B33548
#status         preliminary; nucleic acid sequence not shown; not
                compared with conceptual translation
#molecule_type DNA
#residues       1-126 #label KIP
#experimental_source the sequence was determined from the
                differentiated gene
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        15-98
                #domain immunoglobulin homology #label IMM
SUMMARY        #length 126 #molecular_weight 13710 #checksum 4068

Query Match      59.2%; Score 533; DB 7; Length 126;
Best Local Similarity 74.2%; Pred. No. 1,856-81;
Matches          95; Conservative 14; Mismatches 17; Indels 2; Gaps 2;

Db      1 qvqlv-qsgaevkpkssvkscasggtfssyaiswvraqpgqlwmggiipifgtan 59
QY      1 EVQLLESGAEVKKPKSSSVKSVKASGGTFSGHVSWVPQAPQGLWMMGGSSISFFGTSN 60
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      60 yaqkfgrvtitadeststymelsslrdsodtavyyycar-vsfgr-vqhyvyyymdvwgi 119
QY      61 SAQKFGPVSITADEASATAYMELSLPSSEDAIYVYCAKPPKPPSSSNCYPPQVWQ 120
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      119 qttvtvss 126
QY      121 GTLVTVSS 128

RESULT      6
ENTRY       PH0953
TITLE       #type fragment
ORGANISM    Ig heavy chain V region (G6+ CLL-SIC) - human (fragment)
DATE        #formal_name Homo sapiens #common_name man
            17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
            16-Aug-1996

ACCESSIONS  PH0953
REFERENCE    Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
            J. Exp. Med. (1992) 175:983-991
            Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
#accession      PH0953
#status         nucleic acid sequence not shown
#molecule_type DNA
#residues       1-135 #label MAR
#experimental_source the sequence was determined from the
                differentiated gene
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        1-30
                #region framework 1\
                #domain immunoglobulin homology #label IMM
                #region complementarity-determining 1\
                #region framework 2\
                #region complementarity-determining 2\
                #region framework 3\
                #region complementarity-determining 3\
                #length 132 #checksum 9232

Query Match      68.2%; Score 624; DB 7; Length 132;
Best Local Similarity 72.2%; Pred. No. 5,446-80;
Matches          96; Conservative 16; Mismatches 15; Indels 6; Gaps 4;

Db      1 qvqlv-qsgaevkpkssvkscasggtfssyaiswvraqpgqlwmggiipifgtan 59
QY      1 EVQLLESGAEVKKPKSSSVKSVKASGGTFSGHVSWVPQAPQGLWMMGGSSISFFGTSN 60
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      60 yaqkfgrvtitadeststymelsslrdsodtavyyycarphasididfwgvyvyyvym 119
QY      61 SAQKFGPVSITADEASATAYMELSLPSSEDAIYVYCAKPPKPPSSSNCYPPKPP 115
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      120 dvwtqgtttvss 132
QY      117 Q-W5-GILVTVSS 123

RESULT      8
ENTRY       S46394
TITLE       #type complete
ORGANISM    Ig heavy chain V region - human
DATE        #formal_name Homo sapiens #common_name man
            27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change
            23-May-1997

ACCESSIONS  S46394
REFERENCE    Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
            J. Mol. Biol. (1994) 239:68-78
            In vitro assembly of repertoires of antibody chains on the
            surface of phage by renaturation.
#accession      S46394

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SUMMARY      #length 135 #checksum 2318

Query Match      68.3%; Score 625; DB 7; Length 135;
Best Local Similarity 70.5%; Pred. No. 3,746-80;
Matches          89; Conservative 14; Mismatches 5; Indels 4; Gaps 3;

Db      1 qvqlv-qsgaevkpkssvkscasggtfssyaiswvraqpgqlwmggiipifgtan 59
QY      1 EVQLLESGAEVKKPKSSSVKSVKASGGTFSGHVSWVPQAPQGLWMMGGSSISFFGTSN 60
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      60 yaqkfgrvtitadeststymelsslrdsodtavyyycarng--yo-ggdcys 108
QY      61 SAQKFGPVSITADEASATAYMELSLPSSEDAIYVYCAKPPKPPSSSNCYPP 112
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT      7
ENTRY       PH0954
TITLE       #type fragment
ORGANISM    Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
DATE        #formal_name Homo sapiens #common_name man
            17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
            16-Aug-1996

ACCESSIONS  PH0954
REFERENCE    Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
            J. Exp. Med. (1992) 175:983-991
            Evidence for somatic selection of natural autoantibodies
            #cross-references MUID:92202880
#accession      PH0954
#status         nucleic acid sequence not shown
#molecule_type DNA
#residues       1-132 #label MAR
#experimental_source the sequence was determined from the
                differentiated gene
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        1-30
                #region framework 1\
                #domain immunoglobulin homology #label IMM
                #region complementarity-determining 1\
                #region framework 2\
                #region complementarity-determining 2\
                #region framework 3\
                #region complementarity-determining 3\
                #length 132 #checksum 9232

Query Match      68.2%; Score 624; DB 7; Length 132;
Best Local Similarity 72.2%; Pred. No. 5,446-80;
Matches          96; Conservative 16; Mismatches 15; Indels 6; Gaps 4;

Db      1 qvqlv-qsgaevkpkssvkscasggtfssyaiswvraqpgqlwmggiipifgtan 59
QY      1 EVQLLESGAEVKKPKSSSVKSVKASGGTFSGHVSWVPQAPQGLWMMGGSSISFFGTSN 60
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      60 yaqkfgrvtitadeststymelsslrdsodtavyyycarphasididfwgvyvyyvym 119
QY      61 SAQKFGPVSITADEASATAYMELSLPSSEDAIYVYCAKPPKPPSSSNCYPPKPP 115
        :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      120 dvwtqgtttvss 132
QY      117 Q-W5-GILVTVSS 123

RESULT      8
ENTRY       S46394
TITLE       #type complete
ORGANISM    Ig heavy chain V region - human
DATE        #formal_name Homo sapiens #common_name man
            27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change
            23-May-1997

ACCESSIONS  S46394
REFERENCE    Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
            J. Mol. Biol. (1994) 239:68-78
            In vitro assembly of repertoires of antibody chains on the
            surface of phage by renaturation.
#accession      S46394

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##status preliminary
##molecule_type DNA
##residues 1-132 ##label FIG
##cross-references EMBL:Z31681
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98
SUMMARY
#domain immunoglobulin homology #label IMM
#length 132 #molecular-weight 14293 #checksum 7515

Query Match
Best Local Similarity 72.1%; Score 614; DB 7; Length 132;
Matches 96; Conservative 17; Mismatches 14; Indels 6; Gaps 5;

Db 1 qvqlv-qsgaevkpgssvkscasqgtfssyaiswvraqpgqglewmqgllpifgtan 59
QY 1 EVQLLEQSGAEVKKPGSSVKVKSCASGDTFGHVISWVRQAPGQGLEWMGGSISFFGTSN 60
Db 60 haqkfgarvtitadeststymelsslrdsatvyycaaktgllpysyqpsdyyyv 119
QY 61 SAQKFGQGRVSIADASASTAYMELSLRSEDATYYCAKDP--PRFCSGG--NCYPGFF--Q 116
Db 120 dvwqgqgtttvss 132
QY 117 Q-WGQGLTVTVSS 128

RESULT 9
ENTRY C33548 #type complete
TITLE Ig heavy chain V-1 region (783) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
16-Aug-1996
ACCESSIONS C33548
REFERENCE A33548
#authors Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
#title Developmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in chronic lymphocytic leukemia.
#cross-references MUID:89345575
#accession C33548
#status preliminary; nucleic acid sequence not shown, not compared with conceptual translation
##molecule_type DNA
##residues 1-133 ##label KIP
##experimental_source the sequence was determined from the differentiated gene
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98
SUMMARY
#domain immunoglobulin homology #label IMM
#length 133 #molecular-weight 14320 #checksum 1269

Query Match
Best Local Similarity 73.9%; Score 611; DB 7; Length 133;
Matches 99; Conservative 12; Mismatches 16; Indels 7; Gaps 5;

Db 1 qvqlv-qsgaevkpgssvkscasqgtfssyaiswvraqpgqglewmqgllpifgtan 59
QY 1 EVQLLEQSGAEVKKPGSSVKVKSCASGDTFGHVISWVRQAPGQGLEWMGGSISFFGTSN 60
Db 60 yaqkfgarvtitadeststymelsslrdsatvyycaaktgllpysyqpsdyyyv 119
QY 61 SAQKFGQGRVSIADASASTAYMELSLRSEDATYYCAKDP--PRFCSCG--GNC-YPGFF- 114
Db 120 mdvqgqgtttvss 133
QY 115 FQWGGGLTVTVSS 128

RESULT 10

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ENTRY S14683 #type complete
TITLE Ig mu chain precursor; membrane bound (clone 201) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
16-Aug-1996
ACCESSIONS S14683; S08047
REFERENCE S14683
#authors Friedlander, R.M.; Nussenzeig, M.C.; Leder, P.
#journal Nucleic Acids Res. (1990) 18:4278
#title Complete nucleotide sequence of the membrane form of the human IgM heavy chain.
#cross-references MUID:90332450
#accession S14683
##molecule_type mRNA
##residues 1-627 ##label FRI
##cross-references EMBL:X17115
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS immunoglobulin, membrane protein
FEATURE
1-15 #domain signal sequence #status predicted #label SIGN
16-627 #product Ig mu chain #status predicted #label MAIN
34-117 #domain immunoglobulin homology #label IMM
SUMMARY #length 627 #molecular-weight 68510 #checksum 8581

Query Match 66.8%; Score 611; DB 7; Length 627;
Best Local Similarity 73.9%; Pred. No. 7.13e-78;
Matches 99; Conservative 12; Mismatches 16; Indels 7; Gaps 5;

Db 20 qvqlv-qsgaevkpgssvkscasqgtfssyaiswvraqpgqglewmqgllpifgtan 78
QY 1 EVQLLEQSGAEVKKPGSSVKVKSCASGDTFGHVISWVRQAPGQGLEWMGGSISFFGTSN 60
Db 79 yaqkfgarvtitadeststymelsslrdsatvyycaaktgllpysyqpsdyyyv 138
QY 61 SAQKFGQGRVSIADASASTAYMELSLRSEDATYYCAKDP--PRFCSCG--GNC-YPGFF- 114
Db 139 mdvqgqgtttvss 152
QY 115 FQWGGGLTVTVSS 128

RESULT 11
ENTRY PH0962 #type fragment
TITLE Ig heavy chain V region (G6+ T-142) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
ACCESSIONS PH0962
REFERENCE PH0962
#authors Martin, T.; Duffy, S.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural antinodules.
#cross-references MUID:92202880
#accession PH0962
#status nucleic acid sequence not shown
##molecule_type DNA
##residues 1-120 ##label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-30 #region framework 1N
15-98 #domain immunoglobulin homology #label IMM
31-35 #region complementarity-determining 1N
36-50 #region framework 2N
51-67 #region complementarity-determining 2N
68-98 #region framework 3N
99-108 #region complementarity-determining 3
SUMMARY #length 120 #checksum 5559

Query Match 66.7%; Score 610; DB 7; Length 120;
Best Local Similarity 76.6%; Pred. No. 1.04e-77;
Matches 98; Conservative 12; Mismatches 10; Indels 8; Gaps 5;

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```

Db 1 qvqlv-qsgaevkpgssvkscasqgtfssyaiswvrqpgqgqlwmggllpifqtan 59
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QY 1 EVOLLEQSGAEVKKPGSSVKVSKRSGGTFSGHVISWVRQAPGQGLEWMGSSISFEFTSN 60
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 yqakfggrvtitadeststymelsslsrdsdtavvyccargv---ag-r--p-hfdwgg 112
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SACKFGGRVSIADASATAYMELSSLSRSDTAIYCAKDPDPFPCSGNCTVPGFFQWGO 120
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 113 gtlvtvss 120
  :|||||:
QY 121 gtlvtvss 128

RESULT 12
ENTRY A49590 #type fragment
TITLE Ig heavy chain V region (ACHSV1, clone 15) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
23-May-1997
ACCESSIONS A49590
REFERENCE #authors Burioni, R.; Williamson, R.A.; Sanna, P.P.; Bloom, F.E.;
Burton, D.F.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:355-359
#title Recombinant human Fab to glycoprotein D neutralizes
infectivity and prevents cell-to-cell transmission of
herpes simplex viruses 1 and 2 in vitro
#cross-references MIM:64105168
#accession A49590
#status preliminary; not compared with conceptual translation
#molecule_type nucleic acid
#residues 1-121 #label BUR
#cross-references NCBI:141850
#experimental_source bone marrow lymphocytes
#note #note sequence extracted from NCBI backbone
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
11-94 #domain immunoglobulin homology #label IMM
11-94 #length 121 #checksum 5226
SUMMARY

Query Match 66.6%; Score 603; DB 7; Length 121;
Best Local Similarity 71.3%; Pred. No. 1.51e-77;
Matches 87; Conservative 15; Mismatches 18; Indels 2; Gaps 2.

Db 2 esgaevkpgssvkscstsgatfsyainwvrqapqgqlwmggllpifqtan 61
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 7 QSGAEVKKPGSSVKVSKRSGGTFSGHVISWVRQAPGQGLEWMGSSISFEFTSN 66
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 grvtitadeststymelsslsrdsdtavvyccar-vg-yctngcslgmdvvgggttvi 119
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 67 GRVSIADASATAYMELSSLSRSDTAIYCAKDPDPFPCSGNCTVPGFFQWGO 126
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 ss 121
  :||
QY 127 ss 128

RESULT 13
ENTRY S36261 #type fragment
TITLE Ig heavy chain V region (clone alpha-TNF-E7) - human
(fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
16-Aug-1996
ACCESSIONS S36261
REFERENCE S36256
#authors Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Rye, J.M.;
Embleton, M.J.; McCafferty, J.; Raier, M.; Holliger, K.P.;
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.P.; Winter,
G.
#journal EMBO J. (1993) 12:725-734
#title Human anti-self antibodies with high specificity from phage

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#accession S36261
#status preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-116 #label GRI
#cross-references EMBL:Z18841
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98 #domain immunoglobulin homology #label IMM
15-98 #length 116 #checksum 7971
SUMMARY

Query Match 66.1%; Score 605; DB 7; Length 116;
Best Local Similarity 82.5%; Pred. No. 6.76e-77;
Matches 85; Conservative 11; Mismatches 6; Indels 1; Gaps 1.

Db 1 qvqlv-qsgaevkpgssvkscasqgtfssyaiswvrqpgqgqlwmggllpifqtan 59
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLEQSGAEVKKPGSSVKVSKRSGGTFSGHVISWVRQAPGQGLEWMGSSISFEFTSN 60
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 yqakfggrvtitadeststymelsslsrdsdtavvyccargplr 102
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SACKFGGRVSIADASATAYMELSSLSRSDTAIYCAKDPDPF 103
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
ENTRY PH0959 #type fragment
TITLE Ig heavy chain V region (G6-T-126) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
ACCESSIONS PH0959
REFERENCE Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MIM:92202880
#accession PH0959
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 1-116 #label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-30 #region framework 1\
15-28 #domain immunoglobulin homology #label IMM
31-35 #region complementarity-determining 1\
36-50 #region framework 2\
51-67 #region complementarity-determining 2\
68-98 #region framework 3\
99-104 #region complementarity-determining 3
SUMMARY #length 116 #checksum 5596

Query Match 65.9%; Score 603; DB 7; Length 116;
Best Local Similarity 81.7%; Pred. No. 1.43e-76;
Matches 85; Conservative 11; Mismatches 7; Indels 1; Gaps 1.

Db 1 qvqlv-qsgaevkpgssvkscasqgtfssyaiswvrqpgqgqlwmggllpifqtan 59
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLEQSGAEVKKPGSSVKVSKRSGGTFSGHVISWVRQAPGQGLEWMGSSISFEFTSN 60
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 yqakfggrvtitadeststymelsslsrdsdtavvyccargdnwf 103
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SACKFGGRVSIADASATAYMELSSLSRSDTAIYCAKDPDPF 104
  :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
ENTRY PH0958 #type fragment
TITLE Ig heavy chain V region (G6-T11-98) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
ACCESSIONS PH0958

```

```

REFERENCE
#authors      Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal      J. Exp. Med. (1992) 175:983-991
#title        Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
#accession    PH0958
               #status      nucleic acid sequence not shown
               ##molecule_type DNA
               ##residues     1-122 ##label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
                heterotetramer; immunoglobulin
FEATURE
1-30           #region framework 1\
15-98          #domain immunoglobulin homology #label IMM\
31-35          #region complementarity-determining 1\
36-50          #region framework 2\
51-67          #region complementarity-determining 2\
68-98          #region framework 3\
99-110         #region complementarity-determining 3
SUMMARY        #length 122 #checksum 7292

Query Match      65.7%; Score 601; DB 7; Length 122;
Best Local Similarity 82.9%; Pred. No. 3.02e 76;
Matches 87; Conservative 10; Mismatches 6; Indels 2; Gaps 2;

Db      1 qqlv-qsgaevkpgssvkvscasqgtfssyaiswvraqpqqglewmggiipifgtan 59
QY      1 :||||: ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
        1 EVOLLEQSGAEVKKPGSSVKVSKASGGTFSGHVISWVRQAPQGLEWMGGSISPFPGTSN 60

Db      60 yackfggrvtitadeststaymelsslrsestavyycarvpnpplf 104
QY      1 :||||: ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
        61 SAQKFGGRVSIITADESASTAYWELSSLRSEDTAIYYCAKDP-PRF 104

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Search completed: Tue Feb 24 07:07:53 1998
Job time : 30 secs.

WIRELESS

(TM)

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Distribution rights by IntelliGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on Tue Feb 24 07:15:05 1998: MaxPar time 3.29 seconds
Tabular output not generated. 198.618 Million cell updates/sec

Title: >US-08-844-215-3
Description: (1-128) from US08844215.pep
Perfect Score: 915
Sequence: 1 EVQLLEQSGAEVKKPKSSVK.....NCYPGFFQGWGGILVTVSS 128
Scoring table: PAM 150
Gap 11
Searched: 56402 seqs, 5095871 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1-back1 2.51 3.52 4.53 5.54 6.55 7.56 8 PCT00 9-PCT01
10-PCT02 11-PCT03 12-PCT04 13-PCT05 14-PCT06
Statistics: Mean 28.046; Variance 135.560; scale 0.207

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length DB	ID	Description	Pred No.	
1	628	68.6	129	13	PCT-US95-0 Sequence 45, Applicati	3,600-44	
2	608	66.4	120	11	PCT-US93-1 Sequence 13, Applicati	1,930-42	
3	606	66.2	120	11	PCT-US93-1 Sequence 12, Applicati	2,880-42	
4	585	63.9	147	6	US-08-211-7 Sequence 4, Applicati	1,870-40	
5	560	61.2	102	10	PCT-US92-0 Sequence 55, Applicati	2,680-38	
6	560	61.2	102	10	PCT-US92-1 Sequence 63, Applicati	2,680-38	
7	560	61.2	102	10	PCT-US92-1 Sequence 63, Applicati	2,680-38	
8	560	61.2	102	13	PCT-US95-0 Sequence 2, Applicati	5,930-38	
9	556	60.8	122	13	PCT-US95-0 Sequence 15, Applicati	1,080-37	
10	553	60.4	117	6	US-08-474-7 Sequence 4, Applicati	1,080-37	
11	553	60.4	117	6	US-08-477-7 Sequence 15, Applicati	1,080-37	
12	553	60.4	117	6	US-08-477-7 Sequence 15, Applicati	1,080-37	
13	553	60.4	117	6	US-08-477-7 Sequence 15, Applicati	1,080-37	
14	553	60.4	117	6	US-08-477-7 Sequence 15, Applicati	1,080-37	
15	553	60.4	117	6	US-08-477-7 Sequence 15, Applicati	1,080-37	
16	553	60.4	117	6	US-08-477-7 Sequence 15, Applicati	1,080-37	
17	553	60.4	117	6	US-08-477-7 Sequence 15, Applicati	1,080-37	
18	553	60.4	117	6	US-08-477-7 Sequence 15, Applicati	1,080-37	
19	553	60.4	117	6	US-08-477-7 Sequence 15, Applicati	1,080-37	
20	553	60.4	117	6	US-08-477-7 Sequence 15, Applicati	1,080-37	
21	553	60.4	117	6	US-08-477-7 Sequence 15, Applicati	1,080-37	
22	553	60.4	117	6	US-08-477-7 Sequence 15, Applicati	1,080-37	

23	553	60.4	117	7	US-08-487-7 Sequence 4, Applicati	1,080-37
24	553	60.4	117	7	US-08-487-7 Sequence 104, Applicati	1,080-37
25	553	60.4	117	7	US-08-474-7 Sequence 8, Applicati	1,080-37
26	546	59.7	121	11	PCT-US93-1 Sequence 12, Applicati	4,310-37
27	546	59.7	140	11	PCT-US93-1 Sequence 63, Applicati	4,310-37
28	546	59.7	129	7	US-08-479-7 Sequence 63, Applicati	4,310-37
29	546	59.7	129	7	US-08-479-7 Sequence 63, Applicati	4,310-37
30	546	59.7	129	7	US-08-479-7 Sequence 63, Applicati	4,310-37
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32	546	59.7	129	7	US-08-479-7 Sequence 63, Applicati	4,310-37
33	546	59.7	129	7	US-08-479-7 Sequence 63, Applicati	4,310-37
34	546	59.7	129	7	US-08-479-7 Sequence 63, Applicati	4,310-37
35	546	59.7	129	7	US-08-479-7 Sequence 63, Applicati	4,310-37
36	546	59.7	129	7	US-08-479-7 Sequence 63, Applicati	4,310-37
37	546	59.7	129	7	US-08-479-7 Sequence 63, Applicati	4,310-37
38	546	59.7	129	7	US-08-479-7 Sequence 63, Applicati	4,310-37
39	546	59.7	129	7	US-08-479-7 Sequence 63, Applicati	4,310-37
40	546	59.7	129	7	US-08-479-7 Sequence 63, Applicati	4,310-37
41	546	59.7	129	7	US-08-479-7 Sequence 63, Applicati	4,310-37
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43	546	59.7	129	7	US-08-479-7 Sequence 63, Applicati	4,310-37
44	546	59.7	129	7	US-08-479-7 Sequence 63, Applicati	4,310-37
45	546	59.7	129	7	US-08-479-7 Sequence 63, Applicati	4,310-37

ALIGNMENTS

RESULT 1
ID PCT-US95-01219-45 STANDARD: PRT: 129 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 45, Application PC/TUS9501219.
XX
CC Sequence 45, Application PC/TUS9501219
CC GENERAL INFORMATION:
CC APPLICANT: Pending, Mary M
CC APPLICANT: Leger, Olivier J.
CC APPLICANT: Saldanha, Jose
CC APPLICANT: Jones, S. Tarran
CC TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
CC TITLE OF INVENTION: Adhesion Molecule VLA-4
CC NUMBER OF SEQUENCES: 45
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC City: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/01219
CC FILING DATE: 25-JAN-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/184,264
CC FILING DATE: 25-JAN-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William L.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 15270-14
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9600
CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 45:
CC SEQUENCE CHARACTERISTICS:

CC	TOPOLOGY:	linear	MOLECULE TYPE:	peptide
CC	TOPOLOGY:	linear	MOLECULE TYPE:	peptide
CC	TOPOLOGY:	linear	MOLECULE TYPE:	peptide

CC IMMEDIATE SOURCE:
 CC CLONE: BOR
 CC FEATURE:
 CC NAME/KEY: Peptide
 CC LOCATION: 1..120
 CC SEQUENCE 120 AA; 12984 MW; 80846 CN;

Query Match 66 24; Score 606; DR 11; Length 120;
 Best Local Similarity 74 44; Prod No 2 44a-42;
 Matches 95; Conservative 15; Mismatches 10; Indels 7; Gaps 5;

Db 1 VOLV-QSGAEVKKPGSSVVKVCKASGDTFSSAISVWROAPGQGLEWGGIPIFGTNY 59
 QY 2 VOLV-QSGAEVKKPGSSVVKVCKASGDTFSSAISVWROAPGQGLEWGGIPIFGTNS 61
 Db 60 AQKFGQVITTDSTSTAYMEVSSLPSEDALTYICAPEGRPM-AI-N--P--FYWGGG 113
 QY 62 AQKFGQVITADESTAYMELSSLPSEDALTYICAPEGRPM-AI-N--P--FYWGGG 121
 Db 114 TLTVSS 120
 QY 122 TLTVSS 128

RESULT 4
 ID US-08-217-918-4 STANDARD; PPT; 147 AA.
 XX
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 4, Application US/08217918
 XX
 CC Sequence 4, Application US/08217918
 CC Patent No. 5506132
 CC GENERAL INFORMATION:
 CC APPLICANT: LAKE, PHILIP
 CC APPLICANT: OSTBERG, LARS
 CC TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
 CC TITLE OF INVENTION: VAPICELLA-ZOSTER VIRUS
 CC NUMBER OF SEQUENCES: 4
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESS: Townsend and Townsend Kourie and Crew
 CC STREET: 379 Lytton Avenue
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94301
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC OPERATING SYSTEM: IBM PC compatible
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/217,918
 CC FILING DATE: 24-MAR-1994
 CC CLASSIFICATION: 530
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M
 CC REGISTRATION NUMBER: 30,223
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 326-2400
 CC TELEFAX: (415) 326-2422
 CC INFORMATION FOR SEQ ID NO: 4:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 147 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 147 AA; 15601 MW; 123306 CN;

Query Match 63 48; Score 585; DR 6; Length 147;
 Best Local Similarity 70 28; Prod No 1 87a-40;

Matches 92; Conservative 15; Mismatches 18; Indels 6; Gaps 5;

Db 20 QVALV-QSGAEVKKPGSSVVKVCKASGDTFSSAISVWROAPGQGLEWGGIPIFGT 78
 QY 1 EVQLLESGAEVKKPGSSVVKVCKASGDTFSSAISVWROAPGQGLEWGGIPIFGT 60
 Db 79 YAKFEUGKVTISALASISTAYMELSSLPSEDALTYICAPEGRPM-AI-N--P--FYWGGG 136
 QY 41 SAQFQGVITADESTAYMELSSLPSEDALTYICAPEGRPM-AI-N--P--FYWGGG 117
 Db 137 WGQGITVTVSS 147
 QY 118 WGQGITVTVSS 128

RESULT 5
 ID PCT-US92-06185-55 STANDARD; PPT; 102 AA.
 XX
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 55, Application PC/TUS9206185.
 XX
 CC Sequence 55, Application PC/TUS9206185
 CC GENERAL INFORMATION:
 CC APPLICANT: Lonberg, Nils
 CC APPLICANT: Kay, Robert M.
 CC TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
 CC TITLE OF INVENTION: Producing Heterologous Antibodies
 CC NUMBER OF SEQUENCES: 75
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: William M. Smith
 CC STREET: One Market Plaza, Stewart Tower, Suite 2000
 CC CITY: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US92/06185
 CC FILING DATE: 19910828
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 87654
 CC REFERENCE/DOCKET NUMBER: 14643-5
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-543-9600
 CC TELEFAX: 415-543-5043
 CC INFORMATION FOR SEQ ID NO: 55:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 102 amino acids
 CC TYPE: AMINO ACID
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE 102 AA; 10940 MW; 55781 CN;

Query Match 61 24; Score 560; DR 10; Length 102;
 Best Local Similarity 80 99; Prod No 2 68e-38;
 Matches 80; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

Db 5 QVALV-QSGAEVKKPGSSVVKVCKASGDTFSSAISVWROAPGQGLEWGGIPIFGT 63
 QY 1 EVQLLESGAEVKKPGSSVVKVCKASGDTFSSAISVWROAPGQGLEWGGIPIFGT 60
 Db 54 YAKFEUGKVTISALASISTAYMELSSLPSEDALTYICAPEGRPM-AI-N--P--FYWGGG 120

CC APPLICANT: Kay, Robert M
 CC TITLE OF INVENTION: Transgenic No. 553425-Human Animals Capable of
 CC TITLE OF INVENTION: Producing Heterologous Antibodies
 CC NUMBER OF SEQUENCES: 77
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: William M. Smith
 CC STREET: One Market Plaza, Stewart Tower, Suite 2000
 CC CITY: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/07/834,539A
 CC FILING DATE: 19920205
 CC CLASSIFICATION: 800
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 14643-5
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-543-9600
 CC TELEFAX: 415-543-5043
 CC INFORMATION FOR SEQ ID NO: 55:
 CC SEQUENCE CHARACTERISTICS
 CC LENGTH: 102 amino acids
 CC TYPE: AMINO ACID
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE: 102 AA, 10340 MW, 55761 CN

Query Match 61 24, Score 560, DB 7, Length 102,
 Best Local Similarity 80.8%, Pred. No. 2, 682-34
 Matches 80; Conservative 11; Mismatches 7; Indels 1; Gaps 1

Db 5 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSYVAISWVQAPGQGLEWMGCPPIPIGIAN 63
 QY 1 EVQLLESGAEVKKPGSSVKVSCKASGGTFSGHVSVWVQAPGQGLEWMGSSISFECTEN 60

Db 64 YAKFGQGRVITADKSTAYMELSSLSRPTAVYYCAP 102
 QY 1 EVQLLESGAEVKKPGSSVKVSCKASGGTFSGHVSVWVQAPGQGLEWMGSSISFECTEN 60

Db 61 SAKKFGQGRVITADKSTAYMELSSLSRPTAVYYCAP 99
 QY 1 EVQLLESGAEVKKPGSSVKVSCKASGGTFSGHVSVWVQAPGQGLEWMGSSISFECTEN 60

RESULT 9
 ID PCT-US95-00067-2 STANDARD: PFI: 122 AA
 XX AC xxxxxx
 XX AC xxxxxx
 DT 01-JAN-1990
 XX Sequence 2, Application PC/TUS9500067
 CC GENERAL INFORMATION:
 CC APPLICANT: THE SCRIPTS RESEARCH INSTITUTE
 CC TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPPEPS
 CC TITLE OF INVENTION: SIMPLEX VIRUS AND ANTIBODIES THEREFOR
 CC NUMBER OF SEQUENCES: 25
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Juhas & Lubitz
 CC STREET: 1880 Century Park East, Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/00067
 CC FILING DATE: 04-JAN-1995
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Halle, Ph D., Lisa A.
 CC REGISTRATION NUMBER: 38,347
 CC REFERENCE/DOCKET NUMBER: PD-3229
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 2:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 122 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC IMMEDIATE SOURCE:
 CC CLONE: FdHSV 8
 CC FEATURE:
 CC NAME/KEY: Peptide
 CC LOCATION: 1-122
 CC SEQUENCE: 122 AA, 12999 MW, 86543 CN

Query Match 60 84, Score 556, DB 13, Length 122,
 Best Local Similarity 56.9%, Pred. No. 5, 94e-38;
 Matches 83; Conservative 20; Mismatches 19; Indels 2; Gaps 2

Db 1 LEQSGAEVKKPGSSVKVSCKASGGTFSYVAISWVQAPGQGLEWMGLMPTFGTINVAQK 60
 QY 5 LEQSGAEVKKPGSSVKVSCKASGGTFSGHVSVWVQAPGQGLEWMGSSISFEGTNSAQK 54

Db 61 FQDLITITADVSTAYMELSLGTYETAYYYCAP-VA-YMPEPTVAGGIDWGGQITV 118
 QY 65 FQSGVSTADGASATAYMELSLGTYETAYYYCAP-VA-YMPEPTVAGGIDWGGQITV 124

Db 119 TVAS 122
 QY 125 TVSS 128

RESULT 10
 ID US-08-474-040-15 STANDARD: PFI: 117 AA
 XX AC xxxxxx
 XX AC xxxxxx
 DT 01-JAN-1990
 XX Sequence 15, Application US/08474040
 CC Sequence 15, Application US/08474040
 CC Patent No. 5693761
 CC GENERAL INFORMATION:
 CC APPLICANT: QUEEN, Gary L.
 CC APPLICANT: CO. Man Sung
 CC APPLICANT: SCHNEIDER, William P.
 CC APPLICANT: LANDOLFI, Nicholas F.
 CC APPLICANT: COELINGH, Kathleen L.
 CC APPLICANT: SELICK, Harold E.
 CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 CC NUMBER OF SEQUENCES: 113
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend Kourie and Crew
 CC STREET: 379 Lytton Avenue
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94301
 CC COMPUTER READABLE FORM:

CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: Townsend and Townsend and Crew LLP
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94111
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent In Release #1 0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US 07/477,728
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC TOPOLOGY: unknown
CC STRANDEDNESS: single
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: NO
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1 117
CC OTHER INFORMATION: /note="Pu heavy chain amino acid
CC OTHER INFORMATION: sequence"
SQ SEQUENCE 117 AA; 12472 MW; 77871 CN;

Query Match 60.4%; Score 553; DB 6; Length 117;
Best Local Similarity 80.6%; Pred. No. 1.08e-37;
Matches 79; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

Db 1 QVQLV-DSGAEVKKPGSSVKVSKASGGTSPSAIIHWPAQPGGLEWMGGIVPMPGPPN 59
QY 1 EVQLLESGAEVKKPGSSVKVSKASGGTSPSAIIHWPAQPGGLEWMGGISLFPSTGN 60
DB 60 YAKQFGQGVITADESTNTAYMELSSLRSEDATFYFCA 97
QY 61 SAQKFGQGVITADESTNTAYMELSSLRSEDATFYFCA 98

RESULT 13
ID US-08-477-728-72 STANDARD: PRT: 117 AA.
XX
AC xxxxxx
XX

DI 01-JAN-1990
XX Sequence 72, Application US/08477728.
DE Sequence 72, Application US/08477728
XX Patent No. 5585089
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: Townsend and Townsend and Crew LLP
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94111
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent In Release #1 0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US 07/477,728
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 72:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
SQ SEQUENCE 117 AA; 12472 MW; 77871 CN;

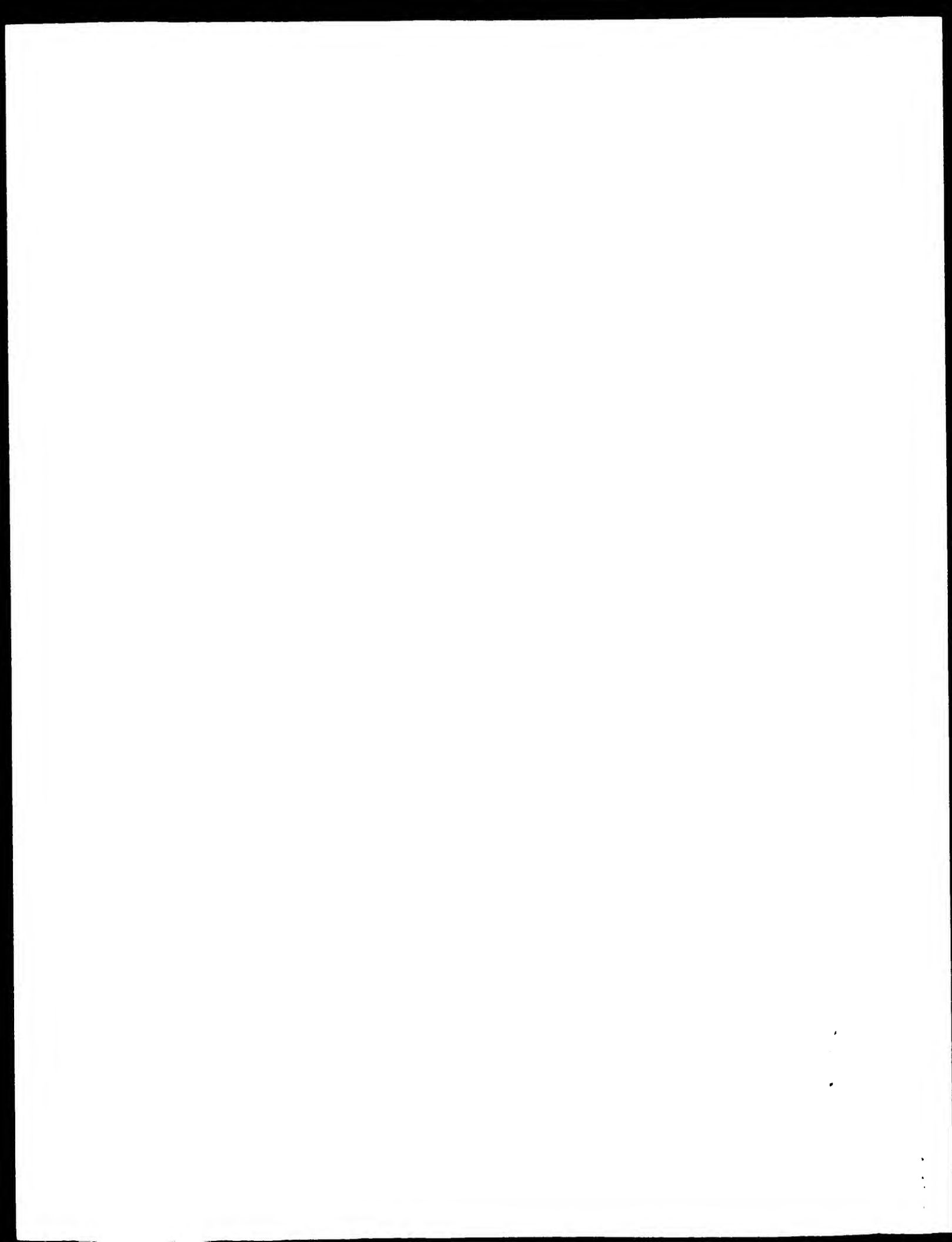
Query Match 60.4%; Score 553; DB 6; Length 117;
Best Local Similarity 80.6%; Pred. No. 1.08e-37;
Matches 79; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

Db 1 QVQLV-DSGAEVKKPGSSVKVSKASGGTSPSAIIHWPAQPGGLEWMGGIVPMPGPPN 59
QY 1 EVQLLESGAEVKKPGSSVKVSKASGGTSPSAIIHWPAQPGGLEWMGGISLFPSTGN 60
DB 60 YAKQFGQGVITADESTNTAYMELSSLRSEDATFYFCA 97
QY 61 SAQKFGQGVITADESTNTAYMELSSLRSEDATFYFCA 98

RESULT 14
ID US-07-634-278-15 STANDARD: PRT: 117 AA.
XX
AC xxxxxx
XX

Db 1 QVQIV-OSCAEVKKPSSSVKVSCKASGTFSPSRAIIWVPCAPGQGLEWMSGIYVMPGPPN 59
QY 1 EVQLEQSGAEVKKPGSSVKVSCKASGTFSGHVISWVPCAPGQGLEWMSGTSISFPGTSN 60
Db 60 YAKRFQGPVTTITADPSTNTAYMFISSLPSEDTAFYFCA 97
QY 61 SAKRFQGRVSTITADESASTAYMELSLRSEDTAIYYCA 98

Search completed: Tue Feb 24 07:35:16 1998
Job time : 11 secs.



Release 2 ID John F Collins, BioComputing Research Unit,
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Distribution rights by Intellicentrics, Inc

Mpsrch protein . protease sequence . Ser-His-W + Cys + Gly + His

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Run on: Tue Feb 24 07:08:10 1998; MasPar time 7.03 Seconds
252.969 Million cell updates/sec
tabular output not generated.
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Tabular output not generated.

Title:	>US-08-844-215-3
Description:	(1-128) from US08844215.pdf

perfect score: 915

RefSeq score: 913
 Sequence: 1 EVOLLEQSGAEVKKPGSSVK NCYPGFFOOWGOGTLVTVSS 128

Scoring table: PAM 150
Gap 11

searched.
111726 eggs. 1000120 residues.

Post-processing: Minimum Match 0%
Listing first 45 summaries

```
Database:
a-generated30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30
```

Statistics: Mean 30.241; Variance 147.709; scale 0.205

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Query Match	Score	Length	DR	ID	Description	Pred. No.
1	756	82.6	481	5	R34442	Sequence of antibody	9.75e-54
2	608	66.4	120	9	R34796	SPA-reactive IgM heavy	4.58e-41
3	608	66.4	476	6	R31023	Antibody D heavy chain	4.58e-41
4	601	65.7	123	23	W39888	CEA-specific antibody	1.83e-40
5	594	64.9	98	12	T20069	DP10 VH region	7.13e-40
6	593	64.8	123	23	W39887	CEA-specific antibody	8.68e-40
7	592	64.7	123	23	W39881	CEA-specific antibody	1.06e-39
8	591	64.6	123	23	W39889	CEA-specific antibody	1.08e-39
9	588	64.3	123	23	W39886	CEA-specific antibody	2.18e-39
10	585	63.9	147	12	R35019	93RA anti-Varicella	4.16e-38
11	584	63.8	119	23	R35336	Anti-melanoma antibody	5.06e-39
12	578	63.2	120	9	R34795	SPA-reactive IgM heavy	1.64e-39
13	560	61.2	99	12	R20664	HV1263 VH region	5.55e-37
14	560	61.2	117	4	R33358	Protein encoded by th	5.55e-37
15	560	61.2	117	7	R38623	Human heavy chain V r	5.55e-37
16	560	61.2	117	20	W37950	DNA fragment vH42.8	5.55e-37
17	556	60.8	122	14	P59564	HSV-neutralising anti	1.21e-36
18	553	60.4	117	2	R34104	Human antibody Eu hea	2.19e-36
19	553	60.4	119	5	R38742	Heavy chain variable	2.19e-36
20	552	60.2	124	9	R37613	Mouse anti-antibody	1.65e-36

AC	CD	RESULT	3
R31023	standard; protein; 476 AA.		
R31023	19-MAY-1993 (first entry)		
DE	Antibody D heavy chain.		
EW	Heavy, light, chain, antibody; C: monoclonal; peripheral; blood;		
KW	lymphocyte; hepatitis A virus; HAV; sero; positive; patient;		
KW	murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H.		
OS	Synthetic.		
FT	key	Location/Qualifiers	
FT	peptide	1..19	
FT	/note= "Signal peptide"		
FT	Region	20..49	
FT	/label= FR1		
FT	Region	50..54	
FT	/label= CDR1		
FT	Region	55..68	
FT	/label= FR2		
FT	Region	69..84	
FT	/label= CDR2		
FT	Region	85..113	
FT	/label= FR3		
FT	Region	114..121	
FT	/label= CDR3		
FT	Region	122..122	

FT	133...241	
FT	/label= CH1	
FT	Region	242..262
FT	/label= HINGE	
FT	Domain	263..379
FT	/label= CH2	
FT	Domain	380..497
FT	/label= CH3	
FT	EP-523949-A.	
PD	20-JAN-1993.	
PD	14-JUL-1992.	306420.
PF	15-JUL-1991.	GB-015284.
PR	01-AUG-1991.	GB-016594.
PR	23-MAR-1992.	GB-006284.
PA	(WELL) WELLCOME FOUND LTD.	
PI	Grove JS, Lewis AP.	
PI	WPI. 93-019951/03.	
DR	N-PSDB: Q35099.	
PT	Prodn. of recombinant primate antibodies - useful for treating	
PT	infections caused by hepatitis A, B and C, herpes, for	
PT	cytomegalovirus, AIDS, ARC, also treat multiple sclerosis.	
PT	arthritis etc.	
PP	Disclosure: Fig 2: 35pb: English.	
PPS	The sequences given in R31023-24 represent the heavy and light chains	
CC	of Antibody D respectively. Antibody D is a monoclonal antibody which	
CC	was derived from peripheral blood lymphocytes from a hepatitis A virus	
CC	(HAV) sero positive patient. Antibody D is closely related in nature	
CC	to murine antibody B5B3. Total RNA was isolated from antibody D	
CC	expressing cells and polyadenylated RNA was extracted. These polyA	
CC	RNA's were used to prepare a cDNA library which was screened for human	
CC	kappa light (L) chains and two positive clones were detected.	
CC	Further heavy (H) chain clones were also isolated.	
CC	Sequence 476 AA:	
SQ		

	Query Match	66.4%	Score 608;	DB 6;	Length 476;
	Best Local Similarity	70.3%	Pred. No. 4,586-41;		
	Matches	90;	Conservative 15;	Mismatches 22;	Indels 1; Gaps
Db	20	qmcvvr-qsgaevrkkgssvtrscskasggtfsnyaiswrrgppqqlcwmaqlplltgpt	78		
	:				
	:				
Qy	1	EVSLLEQSGAPVYPCSSVYFVSWKASGTFPSHVIISWVYQAPQQLFWMAKSL	60	AFPTTSN	
	:				
Db	79	yscngfgrvtiadtksstahmeltsrlsedlavyyccatdrryqndttdrarvqwdpwqj	148		
	:				
Qy	61	SAQKFGGRVSIITADESASTAYNEUSLSLSENTAIYYCAKDPKCSGNGYVGPFLQWQJ	120		

DT	18-oct-1994	(first entry)
DE	SPA-reactive IgM heavy chain clone BOR.	
KW	SpA domain D; Ig binding region; IgM; B-cell superantigen; sAg;	
KW	superantigen; heavy chain variable region; VH3 restricted antibody;	
KW	VH; protein:A; BOR; B-lymphocyte; vaccine.	
OS	Homo sapiens.	
PN	WO9409818-A.	
PD	11-MAY-1994.	
PF	29-OCT-1993; U10555.	
PR	30-OCT-1992; US-969936.	
PA	(REGC) UNIV CALIFORNIA.	
P1	Silverman GJ;	
DR	WFLI 94-167127/20.	
PT	Stimulating prodn. of variable region gene family restricted	
PT	antibodies through B-cell super-antigen vaccination	
PS	A disclosure; page 77; 130pp; English.	
CC	A B-cell superantigen (sAg) is a fragment of SpA D domain that	
CC	specifically binds the Fab portion of variable region restricted	
CC	antibodies. The sAg is used to enhance production of VH, especially	
CC	VH3, restricted Abs. During attempts to identify sAgs, aa sequences	
CC	(R54784-801) of H chains from Ig reactive with mod-SpA, and aa and	
CC	DNA sequences (954802-16, Q64842-56) of VH regions of SpA binders	
CC	obtained from combinatorial libraries were determined. IgM protein	
CC	BOR is derived from the dermline configuration of a VH gene	
CC	segment.	
SC	Sequence 120 AA:	
	Query Match 63.2%; Score 578; DB 9; Length 120;	
	Best Local Similarity 72.4%; Pred. No. 1 640-38;	
	Matches 9; Conservative 16; Mismatches 12; Indels 7; Gaps	
Db	1 vglv-qsgaevkvpqsskvtkcasdttfsssaisswrrqpacqlwmqitpitqny 59	
QY	
	2 VGLLEQSGAEVKKPGSSVSVASGATFSCHVISWPVPADPQGVLEFWWRGNSISPEGTSNS 61	
Db	60 adlfagartlttdestaymrcssrsedtalpyccardcm-ai-n-p--fdywaqq 11	
QY	
	62 AKRFVSPVSIILACSAE-AIMELISSLFSTATAYYAKNPFFPSGGRCYCFTQWRZCG 12	
Db	114 tlvtvss 120	
QY		
	122 TLTVTSS 128	
RESULT 13		
ID	R72069 standard; Protein: 98 AA.	
IC	P72069;	
DE	26-SEP-1995 (first entry)	
DT	HV1263 VH region.	
DE	Graves ophthalmopathy associated immunoglobulin proteins;	
KW	orbital antigen; monoclonal antibody, heavy chain; H chain;	
KW	variable region; autoimmunity.	
OS	Homo sapiens.	
FH	Key	
OS	Location/Qualifiers	
FT	Region 31...35	
FT	/label= CDR1	
FT	Region 50...66	
FT	/label= CDR2	
PN	WO9508336-A.	
PD	30-MAR-1995.	
PF	22-SEP-1994; U10756.	
FR	22-SEP-1993; QS-124469.	
PA	(NICH-) NICHOLS INST DIAGNOSTICS.	
P1	McLachlan SM, Rapoport B;	
DR	N-PDSB; Q89328.	
PT	Graves' ophthalmopathy-associated monoclonal antibody - produced	
PT	by molecular cloning of immunoglobulin genes by PCR	
PS	A disclosure; page 69; 94pp; English.	
CC	L- and H-chain DNA was amplified by PCR from Graves' orbital	
CC	tissue and clones encoding autoimmune-associated immunoglobulin	
CC	fragments were obtained 13/15 clones of H chain (IgG1) genes	
CC	showed homology to the closest germline genes, IGHJ0 (984427) and	

CC 41123 (Q89328). The DNA (Q89324) and corresp. amino acid
CC (R72070) sequences of the VH region of a representative clone,
CC OF7H1.2, are provided.
SQ Sequence 98 AA;

Sequence 98 AA; SQ

Query Match	61.2%;	Score 500;	DB 12,	Length 98;
Best Local Similarity	80.8%;	Pred. No. 5,55e-37;		
Matches	80;	Conservative 11;	Mismatches 7;	Indels 1; Gaps 1;

Db	1	qqqlv-qsgaevkppqssvkysckasqdtfsyaiswvraqqqqlmwmgrilpilgjan	59
		..	
QY	1	EWLLEUQGAQVKKPGSSVKYKSCASGGIFSGHVIVSWKAPQQLGLEMWGGSISEFGTIN	60
Db	60	yaqkfqqrvttidaktstetaymelssrdsedtavyyvar	9A
QY	61	SACKTQGRVSIITADESASTAYMELSSLRPSSETAIYYCAK	9A

RESULT 14
ID R22358 standard: Protein; 117 AA.
AC R22358;
DT 17-AUG-1992 (first entry)
DE Protein encoded by the human heavy chain V region gene VH49.8.
KW Heavy chain; variable region; VH1 family.

PN
WO9203918-A.
PD
19-MAR-1992.
PF
28-AUG-1991; U06185.

PR 31-AUG-1990: US-575962
PA (GENP.) GENPHARM INT INC.
PI Lonberg N, Kay R;
DR WPI: 92-113962/14.
DF N-PSB: Q22419.
PT immunoglobulin trans:genes - for prodn. of heterologous
PI non-rearranged and/or rearranged Ig chains

The human placental genomic DNA library cloned into the phage vector lambda FIX II was screened with the human VH1 family specific oligonucleotide (see O22418). Phage clone lambda 49.8 was isolated and a 6.1 kb XbaI fragment contg. the variable segment VH49.8 subcloned into pNOC3 to generate plasmid pVH49.8. An 800 bp region of this insert was sequenced. VH49.8 was found to have an open reading frame which encoded the sequence shown..




```

RESULT 4
ID HV03_MOUSE STANDARD: PRT: 120 AA.
AC P01747:
DT 21-JUN-1986 (REL 01, CREATED)
DT 21-JUN-1986 (REL 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (36-65).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
PX MEDLINE: 83131846.
PA SIEKOVITZ M., GEFTER M L., RPOHEUR P., RIBLET R.,
PP MAPSHAK-ROTHSTEIN A.;
PP 7. IMMUNOL. 12:123-132 (1982).
CC 1- FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES
CC THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF
CC THESE V REGIONS HAVE PEAPPANCED TO THE SAME V SEGMENT 142.
DP PIR: A02028; HVMSG7.
DSS: P01789; 6FAB.
KK IMMUNOGLOBULIN V REGION: ANTIHSPONATE ANTIBODY: HYBRIDOMA.
FT NON_TER 120
SQ SEQUENCE 120 AA: 13307 MW: 884802.1 GPC32:

Query Match 50.2% SCORE 467; DB 5; Length 120;
Best Local Similarity 56.3%, Pctd. No. 2,330-76;
Matches 71; Conservative 20; Mismatches 24; Indels 6; Gaps

Ddb 1 vq1-qgsgacivragssvssvsskasyvtytssylnkqkqfqqqlawfaylppqpytky 66
      ||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dcy 2 vcllfpqsgafvkvkssvkvstlvcfctfssptlwmfpgapqgsgfpmwmnltppvntltny 61
      ||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Ddb 60 nekfgkttltvdskssstaymglrstdsavvfcarssvyyq---q-syfydvwqql 11
      ||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||| ||| ||| ||| |||
Dcy 62 aokfkgkrlsttadgststymelsslsrdsatvayfcavrvlfnatrlhtmgfyfhwqql 12
      ||| ||| ||| ||||| ||| ||| ||||| ||| ||| ||| ||| ||| ||| |||

Ddb 115 tltyss 120
      |||||
Dcy 122 lvtvss 127

RESULT 5
ID HV1F_HUMAN STANDARD: PRT: 125 AA.
AC P6326:
DT 01-JAN-1988 (REL 06, CREATED)
DT 01-JAN-1988 (REL 06, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL 06, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-I REGION (NOT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
PX MEDLINE: 86203277.
PA KOJIMA M., KOIDE T., ODANI S., ONO T.;
PP MOL. IMMUNOL. 23:169-174 (1986).
DR PIR: A02025; HVHUMO.
DSS: P01772, 8FAB.
KK IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 107 D SEGMENT.
FT 1-MAIN 108 125 J SEGMENT.
FT DISULFID 24 96 BY SIMILARITY.
FT NON_TER 125 125
SQ SEQUENCE 125 AA: 13579 MW: 674502.3 GPC32:

Query Match 49.4% SCORE 460; DB 5; Length 125;
Best Local Similarity 51.2%, Pctd. No. 8,240-75;
Matches 65; Conservative 25; Mismatches 35; Indels 2; Gaps

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QY 1 EVOLLESGAEVKKPGSSVAVSCQVFGDTESPTIQLWLRQAPGCGPFWGNIPVYNTPN 60
Db 60 ygprsqrfvtdststtvmeltalisdaiyycarga-hysdtdsdsgslpwwgg 118
QY 61 YAKFOGFLSITADOSTSTAYMELSSIPSTAVYFCAPVVPNAIPHTMGVYFDVWGG 120
Db 119 tllivss 125
QY 121 TLTVSS 127

RESULT 6
ID HVIC_HUMAN STANDARD: PPT: 143 AA
AC P01744:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-I REGION (ND) (FRAGMENTS).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
PN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83065234.
FA KENTEN J H, MORGAPD H V, HUGHTON M., DEFRYSHE P B., VINEY J,
FA RELL L O., GOULD H J.
RL PROC. NATL. ACAD. SCI. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 16-142.
FA RENNICH H H., JOHANSSON S G.O., VON RAHR-LINDSTROM H.;
RL (IN) IMMEDIATE HYPERSENSITIVITY: MODERN CONCEPTS AND DEVELOPMENTS,
RL BACH M.K., ED., PP.1-36, MARCEL DEKKER, NEW YORK, (1978).
CC -I- THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PFR: A02026; EIHUND.
DR HSP: P01607; IFGV.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT NON_CONS 4 5
FT SIGNAL 1 15
FT CHAIN 16 143 IG HEAVY CHAIN V REGION (ND).
FT MOD_RES 16 16 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 37 111
FT CONFLICT 17 17 T -> V (IN REF. 2).
FT CONFLICT 49 50 IH -> HI (IN REF. 2).
FT CONFLICT 63 64 VG -> GV (IN REF. 2).
FT CONFLICT 121 121 MISSING (IN REF. 2).
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 16051 MW; 6D605E13 CRC32;

Query Match 49.28; Score 458; DB 5; Length 143;
Best Local Similarity 53.8%; Pred. No. 2.28e-74;
Matches 70; Conservative 24; Mismatches 31; Indels 5; Gaps 5,

Db 16 qtlv-qsgaevkpgasvrvscasgytfdisy-lhwirqapghalewgvinnsggt 73
QY 1 EVOLLESGAEVKKPGSSVAVSCQVFGDTF-SRYTIQLWLRQAPGCGPFWGNIPVYNTPN 59
Db 74 nyaprfgrvtrmdasfstaymdrlsrtdsdavfycakspdfwddynfdysyldwv 133
QY 60 NYAKFOGFLSITADOSTSTAYMELSSIPSTAVYFCAPV-VI-PNAIPHTMGVYFDVW 117
Db 134 qggtttvss 143
QY 118 QGGLTVSS 127

RESULT 7
ID HV00_MOUSE STANDARD: PPT: 114 AA.
AC P01741:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (ANTI-ARSONATE ANTIBODY).
OS MUS MUSCULUS (MOUSE).

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
PN [1]
RP SEQUENCE.
RX STRAIN-A/J;
RA CAPRA J.D., NISONOFF A.;
RA J. IMMUNOL. 123:279-284(1979).
CC -I- ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF THE IGG1
CC SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V REGION
CC SEQUENCE.
DR PIR: A02022; GIMSA.
DR HSP: P01772; IFGV.
KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12555 MW; 1A027FD CRC32;

Query Match 49.0%; Score 456; DB 5; Length 114;
Best Local Similarity 69.6%; Pred No 6.31e-74;
Matches 71; Conservative 13; Mismatches 16; Indels 2; Gaps 2;

Db 1 evql-qsgaelvkgssvkmkskattgtfssyelywrgapggldlgyissssaypn 59
QY 1 EVOLLESGAEVKKPGSSVAVSCQVFGDTESPTIQLWLRQAPGCGPFWGNIPVYNTPN 60
Db 60 yaqkfgrvtitadostntaymelsslrscdtavvfavrv 101
QY 61 YAKFOGFLSITADOSTSTAYMELSSLRSDTAVYFCA-RVV 101

RESULT 8
ID HV02_MOUSE STANDARD: PPT: 140 AA.
AC P01746:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (93G7).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
PN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-A/J;
RA MEDLINE; 82152818.
RA S.M.S.J., FABBRI T.H., ESTESS P., SLAUGHTER C., TUCKER P.W.,
RA CAPRA J.D.;
RA SCIENCE 216:309-311(1982).
DR EMBL; J00493; GI95007; -.
DR PIR: A02028; HVM5G7.
DR HSP: P01789; 6FAB.
KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY; HYPERICAMA; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION (93G7).
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 0700D5C8 CRC32;

Query Match 48.1%; Score 448; DB 5; Length 140;
Best Local Similarity 55.9%; Pred. No. 3.58e-72;
Matches 71; Conservative 20; Mismatches 30; Indels 6; Gaps 4;

Db 20 evql-qsgaelvragssvkmkskattgtfssyginvkvprgagglewgyipggayin 78
QY 1 EVOLLESGAEVKKPGSSVAVSCQVFGDTESPTIQLWLRQAPGCGPFWGNIPVYNTPN 60
Db 79 ynefkqkttltvdksststaymqrlsrtdsdavvfcar---sh---ygggyafdwgg 133
QY 61 YAKFOGFLSITADOSTSTAYMELSSLRSDTAVYFCAVPIAIPHTMGVYFDVWGG 120
Db 134 tpltvss 140
QY 121 TLTVSS 127

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RESULT 9
ID HV07_MOUSE STANDARD; PRT: 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JUL-1986 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (H1-8 / 186-2)
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE; 81234546.
FA ROTHWELL A L M, PASKIND M, RETH M, IMANISHI-KAPI T, RAJEWSKY K.,
RA BALTIMORE D.;
PL CELL 24:525-637(1981)
CC -1- THE H1-8 MG CHAIN MPNA WAS CLONED FROM A HYBRIDOMA MAKING
CC ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
CC ANTIBODIES).
DR EMBL; J00529; G195115;
DR PIR; AC2034; MMS18.
DR HSP; P01810; IJHL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION (H1-8 / 186-2).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15410 MW; DEB2C7DA CPC32;

Query Match 45.4%; Score 423; DB 5; Length 139;
Best Local Similarity 51.2%; Pred. No. 1,600-66;
Matches 65; Conservative 27; Mismatches 28; Indels 7; Gaps 6;

Db 20 qvql qqqgavpqpqalvskskasytftsydinwkwkqppqqlwqlwlypqqstsk 78
QY 1 FVQIIEGSGAPVKPGSSVKVSCQVETSTFSYTIQWLQAPQGQPEWMNIPVYNIPN 60
Db 79 ynefkkskalttdkpsstajmqdssltssdsayycar--y-d-yysy-fd-wgqg 132
QY 61 YAKRFQGLSITADDTSTAYMEUSSPSEDVAVYFAPVVPINATPHTWYFYFYWGSQ 120
Db 133 tltvss 139
QY 121 TLTIVSS 127

RESULT 10
ID HV52_MOUSE STANDARD; PRT: 117 AA.
AC P06327;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (VH58 AL/A4).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85099340.
FA YANCOPOULOS G.D., ALT F.W.;
RL CELL.40-271-281(1985)
DR EMBL; M13787; G466291;
DR PIR; A02029; HVMSAL.
DR HSP; P01772; IFOR.
KW IMMUNOGLOBULIN V REGION; SIGNAL.

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FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (VH58 AL/A4).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; A50F2B13 CPC32;

Query Match 44.1%; Score 411; DB 5; Length 117;
Best Local Similarity 56.6%; Pred. No. 4,900-64;
Matches 56; Conservative 20; Mismatches 22; Indels 1; Gaps 1;

Db 20 qvql qqqgavpqpqalvskskasytftsydinwkwkqppqqlwqlwlypqqstsk 78
QY 1 EVQLLEGGSAEVKPKPSSSVKVSQVETSTFSYTIQWLQAPQGQPEWMNIPVYNIPN 60
Db 79 ynefkkskalttdkpsstajmqdssltssdsayycar 117
QY 61 YAKRFQGLSITADDTSTAYMEUSSPSEDVAVYFAP 44

RESULT 11
ID HV31_HUMAN STANDARD; PRT: 119 AA.
AC P01770;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (NIF).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE
RX MEDLINE; 77070269.
FA PONTING L H., HILSCHMANN N.;
FA HOPPE SEYLER'S 2 PHYSIOL. CHEM 357:1571-1604(1976).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE; 77070267.
FA DPEKEP L., SCHWAB J., FEICHEL W., HILSCHMANN N.;
FA HOPPE SEYLER'S 2 PHYSIOL. CHEM 357:1515-1540(1976).
CC -1- THIS CHAIN WAS ISOLATED FROM AN 1961 MYELOMA PROTEIN.
DR PIR; A02053; GHUNI.
DR HSP; P01607; IFGV.
KW IMMUNOGLOBULIN V REGION.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13242 MW; 5703CABE CPC32;

Query Match 44.1%; Score 411; DB 5; Length 119;
Best Local Similarity 50.0%; Pred. No. 4,900-64;
Matches 64; Conservative 31; Mismatches 23; Indels 10; Gaps 6;

Db 1 qvqlv-qsggavpqpqslrlislaasnfifsrvtlihwraapqkqlwvva-vmsylpshk 58
QY 1 EVQLLEGGSAEVKPKPSSSVKVSQVETSTFSYTIQWLQAPQGQPEWMNIPVYNIP 49
Db 59 hyadsvgrftrindskntlylmanlprpdavyycaar--trdt---am---flahwaq 111
QY 60 NVACKFQGLSITADDTSTAYMEUSSPSEDVAVYFAPVVPINATPHTWYFYFYWGSQ 119
Db 112 gtlvtvss 119
QY 120 GTIVTSS 127

RESULT 12
ID HV1D_HUMAN STANDARD; PRT: 124 AA.
AC P01760;

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FT SIGNAL      1 19
FT CHAIN      20 117      1G HEAVY CHAIN V REGION (102).
FT DOMAIN     20 49      FRAMEWORK 1.
FT DOMAIN     50 54      COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN     55 68      FRAMEWORK 2.
FT DOMAIN     69 85      COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN     86 117     FRAMEWORK 3.
FT DISULFID    41 115     BY SIMILARITY.
FT NON-TER     117 117
SQ SEQUENCE 117 AA: 12867 MW: 48DD1982 CRC32:

Query Match      43.8%; Score 408; DB 5; Length 117;
Best Local Similarity 58.8%; Pred. No. 2.22e-63;
Matches 57; Conservative 18; Mismatches 21; Indels 1; Gaps 1;

Db 21 vql-qgpqaelvkpgasvkvsckasqyftfsymhwkvkqpgqglwigrhbpsdsdtny 79
QY 2 VQLLEQSGAEVKPGSSVKVSCQVFGDTFSRYTIQLRLQAPQGPWMGNIIIPVYNTNY 61

Db 80 nskfkakatltdkssstaymqllssitsedsavyyca 116
QY 62 AQRFGRLSITADDSTSTAYMELSURSEDYAVYFCA 98

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Search completed: Tue Feb 24 07:04:39 1998
 Job time : 24 secs.


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J. Mol. Biol. (1994) 239:68-78
In vitro assembly of repertoires of antibody chains on the
surface of phage by renaturation.
#journal
#title
#accession S46394
#status preliminary
##molecule_type DNA
##residues 1-132 ##label FIG
##cross-references EMBL:Z31681
CLASSIFICATION #superfamily immunoglobulin V region, immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98
SUMMARY
#domain immunoglobulin homology #label IMM
#length 132 #molecular-weight 14293 #checksum 7515
Query Match 65.0%; Score 605; DB 7; Length 132;
Best Local Similarity 68.4%; Pred. No. 5,95e-67;
Matches 91; Conservative 18; Mismatches 17; Indels 7; Gaps 5;
Db 1 qvqlv-qsgaevkpgssvkvscasggtfssyaiswvrqpgqglewmgiipifgtan 59
QY 1 EVQLLEQSGAEVKKPKSSVKVSCQVFGDTFSPTTIQWLFOAPGQGPENWGNIIPVYNTPN 60
Db 60 haqkfgrvritadeststamelsrlrsedtavvycaktgllqysgswypnsdyvyyg 119
QY 61 YAAKFGRLSITADSTSTAYMELSLRSEDYAVYFCARVTP--NA-IRHTMG--YYF- 114
Db 120 mdwgggtttvss 132
QY 115 DYWGQGLTVTVSS 127
RESULT 9
ENTRY C33548 #type complete
TITLE Ig heavy chain V-1 region (783) - human
ORGANISM Homo sapiens #common_name man
DATE 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
16-Aug-1996
ACCESSION C33548
REFERENCE Kipps, T.J.; Tonhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.;
Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
Developmentally restricted immunoglobulin heavy chain
variable region gene expressed at high frequency in chronic
lymphocytic leukemia.
#cross-references MIM:89345575
#accession C33548
#status preliminary; nucleic acid sequence not shown; not
compared with conceptual translation
##molecule_type DNA
##residues 1-133 ##label KIP
##experimental_source the sequence was determined from the
differentiated gene
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
15-98
SUMMARY
#domain immunoglobulin homology #label IMM
#length 133 #molecular-weight 14350 #checksum 1289
Query Match 64.9%; Score 604; DB 7; Length 133;
Best Local Similarity 67.9%; Pred. No. 8,27e-67;
Matches 91; Conservative 19; Mismatches 16; Indels 8; Gaps 6;
Db 1 qvqlv-qsgaevkpgssvkvscasggtfssyaiswvrqpgqglewmgiipifgtan 59
QY 1 EVQLLEQSGAEVKKPKSSVKVSCQVFGDTFSPTTIQWLFOAPGQGPENWGNIIPVYNTPN 60
Db 60 haqkfgrvritadeststamelsrlrsedtavvycaktgllqysgswypnsdyvyyg 119
QY 61 YAAKFGRLSITADSTSTAYMELSLRSEDYAVYFCARV--VI-P-NAIRHTMG--YYF- 114
Db 120 mdwgggtttvss 133
QY 115 DYWGQGLTVTVSS 127

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QY 115 -DYWGQGLTVTVSS 127
RESULT 10
ENTRY S14683 #type complete
TITLE Ig mu chain precursor, membrane-bound (clone 201) - human
ORGANISM Homo sapiens #common_name man
DATE 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
16-Aug-1996
ACCESSION S14683
REFERENCE Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. (1980) 18:4278
#authors
#journal
#title
#cross-references MIM:90332450
#accession S14683
##molecule_type mRNA
##residues 1-627 ##label FRI
##cross-references EMBL:X17115
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS immunoglobulin; membrane protein
1-15
FEATURE
16-627
34-117
SUMMARY
#domain signal sequence #status predicted #label SIG
#product Ig mu chain #status predicted #label MATN
#domain immunoglobulin homology #label IMM
#length 627 #molecular-weight 68510 #checksum 8581
Query Match 64.9%; Score 604; DB 7; Length 627;
Best Local Similarity 67.9%; Pred. No. 8,27e-67;
Matches 91; Conservative 19; Mismatches 16; Indels 8; Gaps 6;
Db 20 qvqlv-qsgaevkpgssvkvscasggtfssyaiswvrqpgqglewmgiipifgtan 78
QY 1 EVQLLEQSGAEVKKPKSSVKVSCQVFGDTFSPTTIQWLFOAPGQGPENWGNIIPVYNTPN 60
Db 79 yaqkfgrvritadeststamelsrlrsedtavvycaktgllqysgswypnsdyvyyg 118
QY 61 YAAKFGRLSITADSTSTAYMELSLRSEDYAVYFCARV--VI-P-NAIRHTMG--YYF- 114
Db 139 mdwgggtttvss 152
QY 115 -DYWGQGLTVTVSS 127
RESULT 11
ENTRY S44108 #type complete
TITLE Ig heavy chain V-D-J region - human
ORGANISM Homo sapiens #common_name man
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
23-May-1997
ACCESSION S44108
REFERENCE Hawkins, R.E.; Zhu, D.; Orecka, M.; Winter, G.; Hamblin,
I.J.; Stevenson, F.K.
Submitted to the EMBL Data Library, March 1994
Idiotypic vaccination against human B-cell lymphoma: rescue
of variable region gene sequences from biopsy material for
assembly as single chain iv "personal" vaccine.
#accession S44108
#status preliminary
##molecule_type DNA
##residues 1-123 ##label HAW
##cross-references EMBL:Z31397
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
15-98
SUMMARY
#domain immunoglobulin homology #label IMM
#length 123 #molecular-weight 13307 #checksum 1747
Query Match 64.8%; Score 603; DB 7; Length 123;
Best Local Similarity 69.8%; Pred. No. 1,15e-66;
Matches 81; Conservative 17; Mismatches 16; Indels 2; Gaps 2;

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##restudies
I-122; #label: BOR
##cross-references NCBI:141851
##experimental_source bone marrow lymphocytes
##note sequence extracted from NCBI backbone
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
12-95 #domain immunoglobulin homology #label IMM
SUMMARY #length 122 #checksum 7292

Query Match 64.0%; Score 596; DB 7; Length 122;
Best Local Similarity 69.4%; Pred. No. 1,15e-65;
Matches 86; Conservative 17; Mismatches 18; Indels 3; Gaps 2;

Db 1 leesgaevkpgssvkvsckasggtfnnysaiswvraqpggglewmgglpifnrtakyaqh 60
QY 5 LEQSGAEVKPGSSVKVSCQVGFDSFTYTIQWLFPQAPGGPEWMGNIPVYNTPNYAAQK 64
Db 61 fggrrvtitadesttaymelslrsedtaivycargdtifgv--tmgyvamdvwgqgtv 118
QY 65 FQGFLSITADDTSTAYMELSSLPSEDTAVTFPCAPVVPINAIPTHMGYY-FDYWGQGITLV 123
Db 119 tvas 122
QY 124 TVSS 127

RESULT 14
ENTRY S44106 #type complete
TITLE Ig heavy chain V-D-J region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
23-May-1997

ACCESSIONS S44106
REFERENCE S44105
#authors Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
#submission submitted to the EMBL Data Library, March 1994
#description idiotypic vaccination against human B-cell lymphoma: rescue
of variable region gene sequences from biopsy material for
assembly as single chain fv "personal" vaccine.
#accession S44106
#status preliminary
#molecule_type DNA
#residues 1-119 #label HAW
##cross-references EMBL:Z31362
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
13-96 #domain immunoglobulin homology #label IMM
SUMMARY #length 119 #molecule_wc:ght 12847 #checksum 7181

Query Match 62.9%; Score 586; DB 7; Length 119;
Best Local Similarity 70.9%; Pred. No. 3,11e-64;
Matches 83; Conservative 12; Mismatches 21; Indels 1; Gaps 1;

Db 2 lvqsgaevkpgssvkvsckasggtfnnysaiswvraqpggglewmgglpifnrtakyaqh 61
QY 5 LEQSGAEVKPGSSVKVSCQVGFDSFTYTIQWLFPQAPGGPEWMGNIPVYNTPNYAAQK 64
Db 62 fggrrvtitadesttaymelslrsedtaivycargdhsilsyvyttfdywa-gt 117
QY 65 FQGFLSITADDTSTAYMELSSLPSEDTAVTFPCAPVVPINAIPTHMGYYFDYWGQGIT 121
Db 119 tvas 122
QY 124 TVSS 127

RESULT 15
ENTRY S36261 #type fragment
TITLE Ig heavy chain V region (clone alpha-TNF-E7) - human
(fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
16-Aug-1996
ACCESSIONS S36261

```

```

REFERENCE      S36256
#authors      Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.;
               Embleton, M.J.; McCafferty, J.; Baier, M.; Holliger, K.P.;
               Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
               G.
#journal      EMBO J. (1993) 12:725-734
#title        Human anti-self antibodies with high specificity from phage
               display libraries.
#accession    S36261
#status       preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues     1-116 #label GRI
#cross-references EMBL:Z18841
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        15-98
SUMMARY        #domain immunoglobulin homology #label IMM
               #length 116 #checksum 7971

Query Match      62.1%; Score 578; DB 7; Length 116;
Best Local Similarity 69.5%; Pred. No. 4.31e-63;
Matches 82; Conservative 14; Mismatches 19; Indels 3; Gaps 3;

Db      1 qvql-qesgaevkpgssvkvsckasgdtfssvaiswvrgapggglewmggiiipifgtan 59
        . . . . .
QY      1 EVOLLEQSGAEVKKPGSSVKVSCOVFGDTFSRYTIQWLRAQPGGPEWMGNIIIPVYNTFN 60
        . . . . .

Db      60 yaqkfgrvtitadeststaymelsslrstedtavyyccargplr-gydyvy-yymdwvg 115
        . . . . .
QY      61 YAQKFOGRLSITADDSTSTAYMEISSURSEDYVYFCARVVIPIAIDHTMGYYFDYWG 118
        . . . . .

Search completed: Tue Feb 24 07:05:34 1998
Job time : 35 secs.

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W P E R L H

(TW)

Release 2.1D John F. Collins, BioComputing Research Unit,
Copyright (c) 1994, 1995 University of Edinburgh, U.K.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on Tue Feb 24 07:33:22 1998. MaxPar time 3.39 Seconds
Tabular output not generated. 190,958 Million cell updates/sec

Title: >US-08-844-215-2
Description: (1-127) from US08844215.pep
Perfect Score: 931
Sequence: 1 EVQLLEQSGAEVKKPGSSVK HIMGYFDYWGJGLTVSS 127

Scoring table: PAM 150
Gap 11

Searched: 56402 seqs. 5095871 residues

Post-processing: Minimum Match 0*
Lasting first 45 summaries

Database: a-issued
1.back1 2.51 3.52 4.53 5.54 6.55 7.56 8.57 9.58 10.59
10-pct92 11-pct93 12-pct94 13-pct95 14-pct96

Statistics: Mean 26.297 Variance 150.259 Scale 0.180

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	616	66.2	147	6	US-08-217-918-4 Sequence 4, Application	5,456-39
2	603	64.7	120	13	PCT-US95-0 Sequence 12, Applicati	6,856-38
3	583	62.6	129	13	PCT-US95-0 Sequence 45, Applicati	2,136-36
4	579	62.2	120	11	PCT-US93-1 Sequence 13, Applicati	4,406-36
5	565	60.7	122	13	PCT-US95-0 Sequence 2, Applicati	2,536-35
6	551	59.2	128	7	US-08-474- Sequence 63, Applicati	6,936-34
7	550	59.1	102	10	PCT-US92-0 Sequence 63, Applicati	9,336-34
8	550	59.1	102	10	PCT-US92-0 Sequence 55, Applicati	8,306-34
9	550	59.1	102	7	US-07-834- Sequence 12, Applicati	1,196-33
10	548	58.9	140	11	PCT-US93-1 Sequence 3, Applicati	1,716-33
11	545	58.6	121	7	US-08-477- Sequence 104, Applicati	2,936-33
12	545	58.6	121	7	US-08-477- Sequence 15, Applicati	2,936-33
13	545	58.5	121	11	PCT-US93-1 Sequence 15, Applicati	2,936-33
14	543	58.3	117	6	US-08-474- Sequence 104, Applicati	2,936-33
15	543	58.3	117	6	US-08-474- Sequence 15, Applicati	2,936-33
16	543	58.3	117	6	US-08-474- Sequence 15, Applicati	2,936-33
17	543	58.3	117	6	US-08-474- Sequence 15, Applicati	2,936-33
18	543	58.3	117	6	US-08-474- Sequence 15, Applicati	2,936-33
19	543	58.3	117	6	US-08-474- Sequence 15, Applicati	2,936-33
20	543	58.3	117	6	US-08-474- Sequence 15, Applicati	2,936-33
21	543	58.3	117	6	US-08-474- Sequence 15, Applicati	2,936-33
22	543	58.3	117	6	US-08-474- Sequence 15, Applicati	2,936-33

23	543	58.3	117	7	US-08-474- Sequence 72, Applicati	2,936-33
24	543	58.3	117	7	US-08-474- Sequence 4, Applicati	2,936-33
25	543	58.3	117	6	US-08-477- Sequence 72, Applicati	2,936-33
26	543	58.3	117	6	US-08-477- Sequence 104, Applicati	2,936-33
27	543	58.3	117	6	US-08-477- Sequence 4, Applicati	2,936-33
28	543	58.3	117	6	US-07-634- Sequence 72, Applicati	2,936-33
29	543	58.3	117	6	US-07-634- Sequence 104, Applicati	2,936-33
30	538	57.8	121	6	US-08-477- Sequence 53, Applicati	7,236-33
31	538	57.8	121	6	US-07-634- Sequence 53, Applicati	7,236-33
32	538	57.8	121	7	US-08-477- Sequence 53, Applicati	7,236-33
33	538	57.8	121	7	US-08-474- Sequence 53, Applicati	7,236-33
34	514	55.2	123	13	PCT-US95-0 Sequence 11, Applicati	5,456-31
35	514	55.2	123	13	PCT-US95-0 Sequence 17, Applicati	5,456-31
36	502	53.0	140	16	US-07-246- Sequence 28, Applicati	4,726-30
37	502	53.0	140	16	US-07-246- Sequence 155, Applicati	4,726-30
38	502	53.0	140	16	US-07-246- Sequence 155, Applicati	4,726-30
39	501	53.8	124	7	US-08-276- Sequence 66, Applicati	5,646-30
40	501	53.8	124	13	PCT-US95-0 Sequence 66, Applicati	5,646-30
41	496	53.3	119	13	PCT-US95-0 Sequence 10, Applicati	1,396-29
42	495	53.2	119	13	PCT-US95-0 Sequence 10, Applicati	1,396-29
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ALIGNMENTS

RESULT 1 STANDARD: PRT: 147 AA.
ID US-08-217-918-4
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AC xxxxxx
DT 01-JAN-1900
DE Sequence 4, Application US/08217918.
XX
Sequence 4, Application US/08217918
Patent No. 5506132
GENERAL INFORMATION:
APPLICANT: LAKE, PHILIP
ATTORNEY: CSTERG, LARS
TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
TITLE OF INVENTION: VAPICELLA-ZOSTER VIRUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Hourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTA, FASTA-PC, V-SEARCH #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/217,918
FILING DATE: 24-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO. 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 147 AA: 1000 MW, 22300 Cn

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Query Match      64.78, Score 602, DB 13, Length 129;
Best Local Similarity 72.24; Pred. No. 6,85e-38;
Matches 91; Conservative 14; Mismatched 18; Indels 6; Gaps
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14y 2 VALLVSGSAEAKKKKGLSSAVKVSGLVFQTESPTLGMLEAPAGDGFPMWGNIIPVYNIPNY 61
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14b 60 AKKFQGPVTITTDSTSTAMWSVSESDTALYYCAHFGRRMALNP----FYHWGGTI 114
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
14y 62 AKKFQGPSITIAFSTSTAYMELSSISELTAVYCFARPVVIPAIPHMTIMYYFTVMWSQGT 121
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Db 115 LTVSSS 120
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Qy 122 LTVSSS 127

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ID PCT-US95-01219-45 STANDARD: PFI 129 AA.
XX AC
XX xxxxxx
DT 01-JAN-1900
XX Sequence 45, Application PCT/US95-01219.
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CC Sequence 45, Application PCT/US95-01219
CC GENERAL INFORMATION:
CC APPLICANT: Bendig, Mary M.
CC APPLICANT: Leder, Olivier J.
CC APPLICANT: Saldanha, Jose
CC APPLICANT: Jones, S. Tarran
CC TITLE OF INVENTION: Humanized Antibodies Against Insulin p7c
CC TITLE OF INVENTION: Adhesion Molecule VLA-4
CC NUMBER OF SEQUENCES: 45
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Hourie and Crow
CC STREET: One Market Plaza, Stewart Tower Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER PROGRAM: FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: pc-dos/ms-dos
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBR: PCT/US95/01219
CC FILING DATE: 25-JAN-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/186,269
CC FILING DATE: 25-JAN-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William L.
CC REGISTRATION NUMBER: 20,223
CC REFERENCE/CHECK NUMBER: 15270-14
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9400
CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 45:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 129 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 129 AA; 13930 MW; 96169 CN;
SQ

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01 EVOLLEQSGAEVKKPGSSVKVVSCGVFDTETSPYIIHWLFGAPGQGGPFWWNSNIIPVNTN 63
64 YAAKFGQGVITITADKSTISTAYMELSLSESDTAVYYCAR 102
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01 YAAKFGQGLSITADDSITAYMELSLSEPSDTSVTAVFCAR 99
      :|||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
ID US-08-053-131-63 STANDARD: PRT: 102 AA.
XX xxxxxx
XX
XX 01-JAN-1900
XX DE
DE Sequence 63, Application US/08053131.
XX
XX Sequence 63, Application US/08053131
XX Patent No. 5661016
XX GENERAL INFORMATION.
CC APPLICANT: Kay, Robert M
CC APPLICANT: Lonberg, Nils
CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 197
CC COMPESP/NUMBER ADDRESS.
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: One Market Plaza, Stewart Tower, Suite 200
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER PEACABLE FORM.
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent Release #1 0, Version #1 25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/053,131
CC FILING DATE: 26-APR-1993
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA.
CC APPLICATION NUMBER: US 07/990,860
CC FILING DATE: 16-DEC-1992
CC PRIOR APPLICATION DATA.
CC APPLICATION NUMBER: US 07/910,279
CC FILING DATE: 17-DEC-1991
CC PRIOR APPLICATION DATA.
CC APPLICATION NUMBER: US 07/853,408
CC FILING DATE: 18-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-a-3
CC TELECOMMUNICATION INFORMATION.
CC TELEPHONE: 415-326-3400
CC TELEFAX: 415-326-3420
CC INFORMATION FOR SEQ ID NO: 63.
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 102 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 102 AA; 10340 MW; 55781 CN;
Query Match 59.1%; Score 550; DB 7; Length 102;
Best Local Similarity 77.8%; Pred. No. 8,30e-34;
Matches 77; Conservative 9; Mismatches 12; Indels 1; Gaps

Db 5 OVQLV-QSGAEVKKPGSSVKVSKASGGTSTSSVAISVAKSWPCAGQGLEGWGPPIIPILGTIAN 63
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01 EVOLLEQSGAEVKKPGSSVKVVSCGVFDTETSPYIIHWLFGAPGQGGPFWWNSNIIPVNTN 63
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QY      61 YACKFGRLSIADSTSTAYWELSLPSED7AVYFCAP 99
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XX                                     AC         xxxxxx
XX                                     AC         01-JAN-1900
XX                                     DE         Sequence 55, Application PC/TUS9206185.
XX                                     CC         Sequence 55, Application PC/TUS9206185
XX                                     CC         GENERAL INFORMATION:
XX                                     CC         APPLICANT: Lonberg, Nils
XX                                     CC         TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
XX                                     CC         TITLE OF INVENTION: Producing Heterologous Antibodies
XX                                     CC         NUMBER OF SEQUENCES: 75
XX                                     CC         CORRESPONDENCE ADDRESS:
XX                                     CC         ADDRESSEE: William M. Smith
XX                                     CC         STREET: One Market Plaza, Stewart Tower, Suite 2000
XX                                     CC         CITY: San Francisco
XX                                     CC         STATE: California
XX                                     CC         COUNTRY: USA
XX                                     CC         ZIP: 94105
XX                                     CC         COMPUTER READABLE FORM:
XX                                     CC         MEDIUM TYPE: Floppy disk
XX                                     CC         COMPUTER: IBM PC compatible
XX                                     CC         OPERATING SYSTEM: PC-DOS/MS-DOS
XX                                     CC         SOFTWARE: Patent In Release #1 0, Version #1.25
XX                                     CC         CURRENT APPLICATION DATA:
XX                                     CC         APPLICATION NUMBER: PAT/US92/06185
XX                                     CC         FILING DATE: 19910828
XX                                     CC         CLASSIFICATION:
XX                                     CC         ATTORNEY/AGENT INFORMATION:
XX                                     CC         NAME: Smith, William M.
XX                                     CC         REGISTRATION NUMBER: 87654
XX                                     CC         REFERENCE/DOCKET NUMBER: 14643-5
XX                                     CC         TELECOMMUNICATION INFORMATION:
XX                                     CC         TELEPHONE: 415-543-9600
XX                                     CC         TELEFAX: 415-543-5043
XX                                     CC         INFORMATION FOR SEQ ID NO: 55:
XX                                     CC         SEQUENCE CHARACTERISTICS:
XX                                     CC         LENGTH: 102 amino acids
XX                                     CC         TYPE: AMINO ACID
XX                                     CC         STRANDEDNESS: single
XX                                     CC         TOPOLOGY: linear
XX                                     CC         MOLECULE TYPE: peptide
SQ     SEQUENCE 102 AA; 10940 MW; 55781 CN;

Query Match      59 1%; Score 550; DR 10; Length 102;
Pest Local Similarity 77 8%; Pred No 8.40e-34;
Matches 77, Conservative 9, Mismatches 12, Indels 1, Gaps

Db      5 QVGLV_QSTAQVKKPKSSVKSVKSCASGDTSSVAISNVFPJAPRGSLFWMKRILPIGLGAN 63
      1 EVQLLEQSGAEYKKPGKGVSKVCVFEDITSPKTIQLFLQAPQGQGPENMNTIPVYNTPN 60
QY      61 YAKKPFGRLSIADSTSTAYWELSLPSED7AVYFCAR 99
Db      54 YAKKPFGRVTITADKSTSTAYWELSLPSED7AVYFCAR 102
QY      61 YAKKPFGRLSIADSTSTAYWELSLPSED7AVYFCAR 99

RESULT      10
ID   QS-07-934-539A-55        STANDAPP;       PPT;    102 AA.
XX                                     AC         xxxxxx
XX                                     AC         01-JAN-1900
XX                                     DE         Sequence 55, Application QS/07R34539A

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QY      61 YACKFGRLSIADDSSTAYWELSLPSSDSEDTAVYFCAP 99
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XX                                     AC      xxxxxx
XX                                     AC      01-JAN-1900
XX                                     DE      Sequence 55, Application PC/TUS9206185.
XX                                     CC      Sequence 55, Application PC/TUS9206185
XX                                     CC      GENERAL INFORMATION:
XX                                     CC      APPLICANT: Lonberg, Nils
XX                                     CC      TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
XX                                     CC      TITLE OF INVENTION: Producing Heterologous Antibodies
XX                                     CC      NUMBER OF SEQUENCES: 75
XX                                     CC      CORRESPONDENCE ADDRESS:
XX                                     CC      ADDRESSEE: William M. Smith
XX                                     CC      STREET: One Market Plaza, Stewart Tower, Suite 2000
XX                                     CC      CITY: San Francisco
XX                                     CC      STATE: California
XX                                     CC      COUNTRY: USA
XX                                     CC      ZIP: 94105
XX                                     CC      COMPUTER READABLE FORM:
XX                                     CC      MEDIUM TYPE: Floppy disk
XX                                     CC      COMPUTER: IBM PC compatible
XX                                     CC      OPERATING SYSTEM: PC-DOS/MS-DOS
XX                                     CC      SOFTWARE: Patent In Release #1 0, Version #1.25
XX                                     CC      CURRENT APPLICATION DATA:
XX                                     CC      APPLICATION NUMBER: PAT/US92/06185
XX                                     CC      FILING DATE: 19910828
XX                                     CC      CLASSIFICATION:
XX                                     CC      ATTORNEY/AGENT INFORMATION:
XX                                     CC      NAME: Smith, William M.
XX                                     CC      REGISTRATION NUMBER: 87654
XX                                     CC      REFERENCE/DOCKET NUMBER: 14643-5
XX                                     CC      TELECOMMUNICATION INFORMATION:
XX                                     CC      TELEPHONE: 415-543-9600
XX                                     CC      TELEFAX: 415-543-5043
XX                                     CC      INFORMATION FOR SEQ ID NO: 55:
XX                                     CC      SEQUENCE CHARACTERISTICS:
XX                                     CC      LENGTH: 102 amino acids
XX                                     CC      TYPE: AMINO ACID
XX                                     CC      STRANDEDNESS: single
XX                                     CC      TOPOLOGY: linear
XX                                     CC      MOLECULE TYPE: peptide
SQ     SEQUENCE 102 AA; 10940 MW; 55781 CN;

Query Match      59.1%; Score 550; DR 10; Length 102;
Pest Local Similarity 77.8%; Pred No. 8.30e-34;
Matches 77, Conservative 9, Mismatches 12, Indels 1, Gaps

Db      5 QVGLV_QSTAQVKRKASSVKSVKSCASGDTSSVAISNVFPJAPRGSGLEWHM-KRIPILIGIAN 63
      1 EVQLLEQSGAEYKKGGSKVKVCQAFEDTSPKTIQLFQAQGQGPENMKNTIPYINTPN 60
QY      61 YAKKPFGRLSITADDSSTAYWELSLPSSDSEDTAVYFCAR 99
Db      54 YAKKPFGRVTITADKSTSTAYWELSLPSSDSEDTAVYFCAR 102
QY      61 YAKKPFGRLSITADDSSTAYWELSLPSSDSEDTAVYFCAR 99

RESULT      10
ID   QS-07-934-539A-55        STANDARD;       PRT:    102 AA.
XX                                     AC      xxxxxx
XX                                     AC      01-JAN-1900
XX                                     DE      Sequence 55, Application QS/07934539A
XX                                     CC      Sequence 55, Application QS/07934539A

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US-08-844-215-2-rai

Thu Feb 26 07:04:44 1998

xx Sequence 55, Application US/07834539A
cc Patent No. 5633425
cc GENERAL INFORMATION:
cc APPLICANT: Lonberg, Nils
cc APPLICANT: Kay, Robert M.
cc TITLE OF INVENTION: Transgenic No. 5633425-Human Animals Capable of
cc TITLE OF INVENTION: Producing Heterologous Antibodies
cc NUMBER OF SEQUENCES: 77
cc CORRESPONDENCE ADDRESS:
cc ADDRESSEE: William M. Smith
cc STREET: One Market Plaza, Steuart Tower, Suite 2000
cc CITY: San Francisco
cc STATE: California
cc COUNTRY: USA
cc ZIP: 94105
cc COMPUTER READABLE FORM:
cc MEDIUM TYPE: Floppy disk
cc COMPUTER: IBM PC compatible
cc OPERATING SYSTEM: PC-DOS/MS-DOS
cc SOFTWARE: Patent In Release #1.0, Version #1.25
cc CURRENT APPLICATION DATA:
cc FILING DATE: 07/834,539A
cc APPLICATION NUMBER: 07/834,539A
cc CLASSIFICATION: 800
cc ATTORNEY/AGENT INFORMATION:
cc NAME: Smith, William M.
cc REGISTRATION NUMBER: 30,223
cc REFERENCE/DOCKET NUMBER: 14643-5
cc TELECOMMUNICATION INFORMATION:
cc TELEPHONE: 415-543-9600
cc TELEFAX: 415-543-5043
cc INFORMATION FOR SEQ ID NO: 55:
cc SEQUENCE CHARACTERISTICS:
cc LENGTH: 102 amino acids
cc TYPE: AMINO ACID
cc STRANDEDNESS: single
cc TOPOLOGY: linear
cc MOLECULE TYPE: peptide
cc SEQUENCE 102 AA: 10940 MW: 55781 CN:
Query Match 59.1%; Score 550; DB 7; Length 102;
Best Local Similarity 77.8%; Pred. No. 8.30e-34,
Matches 77; Conservative 9; Mismatches 12; Indels 1; Gaps 1;
Db 5 QVQLV-QSGAEVKPGSSVKVSKASGTFSSYALSWVRQAPGQGLEWMGRILPIIGIAN 63
QY 1 EVQLLEQSGAEVKPGSSVKVSKGVFGDTFSRYTIQWLROAPGGPEWMGNIIPIVNTPN 60
Db 64 YAKKFGKRVITITADKSTSTAYMELSLRSRSEDYAVYYCAR 102
QY 61 YAKKFGKRLSITADSTSTAYMELSLRSRSEDYAVYYCAR 99
RESULT 11
ID PCT-US93-11612-12 STANDARD: PPT: 140 AA.
XX XXXXXX
XX 01-JAN-1900
XX Sequence 12, Application PC/TUS9311612.
DE GENERAL INFORMATION:
CC APPLICANT: Co. Man Sung
CC TITLE OF INVENTION: Humanized Antibodies Reactive with
CC TITLE OF INVENTION: L-Selectin
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khourie and Crew
CC STREET: One Market Plaza, Steuart Tower, Suite 2000
CC CITY: San Francisco

cc STATE: California
cc COUNTRY: USA
cc ZIP: 94105
cc COMPUTER READABLE FORM:
cc MEDIUM TYPE: Floppy disk
cc COMPUTER: IBM PC compatible
cc OPERATING SYSTEM: PC-DOS/MS-DOS
cc SOFTWARE: Patent In Release #1.0, Version #1.25
cc CURRENT APPLICATION DATA:
cc APPLICATION NUMBER: PCT/US93/11612
cc FILING DATE:
cc CLASSIFICATION:
cc PRIOR APPLICATION DATA:
cc APPLICATION NUMBER: US 07/983,946
cc FILING DATE: 01-DEC-1992
cc ATTORNEY/AGENT INFORMATION:
cc NAME: Smith, William M.
cc REGISTRATION NUMBER: 30,223
cc REFERENCE/DOCKET NUMBER: 11823-22
cc TELECOMMUNICATION INFORMATION:
cc TELEPHONE: 415-326-2400
cc TELEFAX: 415-326-2422
cc INFORMATION FOR SEQ ID NO: 12:
cc SEQUENCE CHARACTERISTICS:
cc LENGTH: 140 amino acids
cc TYPE: amino acid
cc TOPOLOGY: linear
cc MOLECULE TYPE: protein
cc SEQUENCE 140 AA: 15650 MW: 117746 CN:
Query Match 58.9%; Score 548; DB 11; Length 140;
Best Local Similarity 65.4%; Pred. No. 1.19e-33;
Matches 83; Conservative 17; Mismatches 21; Indels 6; Gaps 2;
Db 20 QVQLV-QSGAEVKPGSSVKVSKASGTFSSYALSWVRQAPGQGLEWMGRILPIIGIAN 78
QY 1 EVQLLEQSGAEVKPGSSVKVSKGVFGDTFSRYTIQWLROAPGGPEWMGNIIPIVNTPN 60
Db 79 YNEKFKGRVITITADKSTSTAYMELSLRSRSEDYAVYYCAR 144
QY 61 YAKKFGKRLSITADSTSTAYMELSLRSRSEDYAVYYCAR 121
Db 134 TLTVSS 140
QY 121 TLTVSS 127
RESULT 12
ID US-08-264-093-3 STANDARD: PPT: 121 AA.
XX XXXXXX
XX 01-JAN-1900
XX Sequence 3, Application US/08264093.
XX Sequence 3, Application US/08264093
CC Patent No. 5639863
CC GENERAL INFORMATION:
CC APPLICANT: Michael D. Dan
CC TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
CC TITLE OF INVENTION: CELL CYCLIN-INDEPENDENT GLIOMA SURFACE
CC TITLE OF INVENTION: ANTIGEN
CC NUMBER OF SEQUENCES: 26
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Kidout & Maybee
CC STREET: 2400 Richmond-Adelade Centre
CC STREET: 101 Richmond Street West
CC CITY: Toronto
CC STATE: Ontario
CC COUNTRY: Canada
CC ZIP: M5H 2J7
CC COMPUTER READABLE FORM:

* MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264.043
FILING DATE:
CLASSIFICATION: 536
PRPC APPLICATION DATA: No. 5630963 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James P.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVAP/106A/7551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ. ID. NO. 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDNESS: not applicable
TOPOLOGY: linear
SEQUENCE 121 AA: 13281 MW: 86979 CN:

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 XX
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 XX
 01-JAN-1900
 XX
 DE Sequence 8, Application PC/TUS9311612.
 XX
 CC Sequence 8, Application PC/TUS9311612
 CC GENERAL INFORMATION.
 CC APPLICANT: CO, Man Sung
 CC TITLE OF INVENTION: Humanized Antibodies Reactive with
 CC TITLE OF INVENTION: L-Selectin
 CC NUMBER OF SEQUENCES: 12
 CC CORRESPONDENCE ADDRESS.
 CC ADDRESSEE: Townsend and Townsend Khourie and Crew
 CC STREET: One Market Plaza, Stewart Tower, Suite 2000
 CC CITY: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/11612
 CC FILING DATE:
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC

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CC APPLICATION NUMBER: US 07/983,945
CC FILING DATE: 01-DEC-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/EXCIT. NUMBER: 11823-22
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-326-2400
CC TELEFAX: 415-326-2422
CC INFORMATION FOR SEQ ID NO: 9:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 121 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 121 AA: 13661 MW: 87993 CN:

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Best Local Similarity 64.6% Pred. No. 2,056-33:
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      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YAEKFGQPLSTALQSTSTAYMELSSLSPEGTAVYFCARVVPINAPHTMWSYFTWAGT 120
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ID US-08-477-728-104 STANDARDS: PPT; 117 AA.
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XX xxxxxx
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XX 01-JAN-1900
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XX Sequence 104, Application US/08477728.
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XX Sequence 104, Application US/08477728
XX Patent No. 5585089
XX GENERAL INFORMATION:
XX APPLICANT: QUEEN, Cary L.
XX APPLICANT: SCHNEIDER, William P.
XX APPLICANT: SELICK, Harold E.
XX TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
XX NUMBER OF SEQUENCES: 113
XX CORRESPONDENCE ADDRESS:
XX ADDRESSEE: Townsend and Townsend and Crew LLP
XX STREET: Two Embarcadero Center, 8th Floor
XX CITY: Palo Alto
XX STATE: California
XX COUNTRY: US
XX ZIP: 94111
XX COMPUTER READABLE FORM:
XX MEDIUM TYPE: Floppy disk
XX COMPUTER: IBM PC compatible
XX OPERATING SYSTEM: PC-DOS/MS-DOS
XX SOFTWARE: PatentIn Release #1.0, Version #1.25
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: US/08/477,728
XX FILING DATE: 07-JUN-1995
XX CLASSIFICATION: 424
XX
XX PRIOR APPLICATION DATA:
XX APPLICATION NMESEF: US 07/634,278
XX FILING DATE: 19-DEC-1990
XX PRIOR APPLICATION DATA:
XX APPLICATION NUMBER: US 07/590,274

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Thu Feb 26 07:04:44 1998

CC FILING DATE: 28-SEP-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/310,252
 CC FILING DATE: 13-FEB-1989
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/290,975
 CC FILING DATE: 28-DEC-1988
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 11823-002600
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 326-2400
 CC TELEFAX: (415) 326-2422
 CC INFORMATION FOR SEQ ID NO: 104:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 117 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE 117 AA; 12472 MW; 77871 CN;

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 Best Local Similarity 76.5%; Pred No 2 93e-33;
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Db 1 QVQLV-QSGAEVKKPGSSVKVSKASGTFSSRAIIWVRQAPGQGLEWMGGIIVPMFGPPN 59
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RESULT 15
 ID US-08-487-200-72 STANDARD: PPT: 117 AA.
 XX AC xxxxxx
 XX DT 01-JAN-1900
 XX DE Sequence 72, Application US/08487200.
 XX Sequence 72, Application US/08487200.
 CC Patent No. 5693762
 CC GENERAL INFORMATION:
 CC APPLICANT: QUEEN, Cary L.
 CC APPLICANT: CO, Man Sung
 CC APPLICANT: SCHNEIDER, William P.
 CC APPLICANT: LANDOLFI, Nicholas F.
 CC APPLICANT: GOELINGH, Kathleen L.
 CC APPLICANT: SELICK, Harold E.
 CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 CC NUMBER OF SEQUENCES: 113
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend and Crew
 CC STREET: 379 Lytton Avenue
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94301
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/487,200
 CC FILING DATE: 7-JUN-1995
 CC CLASSIFICATION: 424
 CC PRIOR APPLICATION DATA:

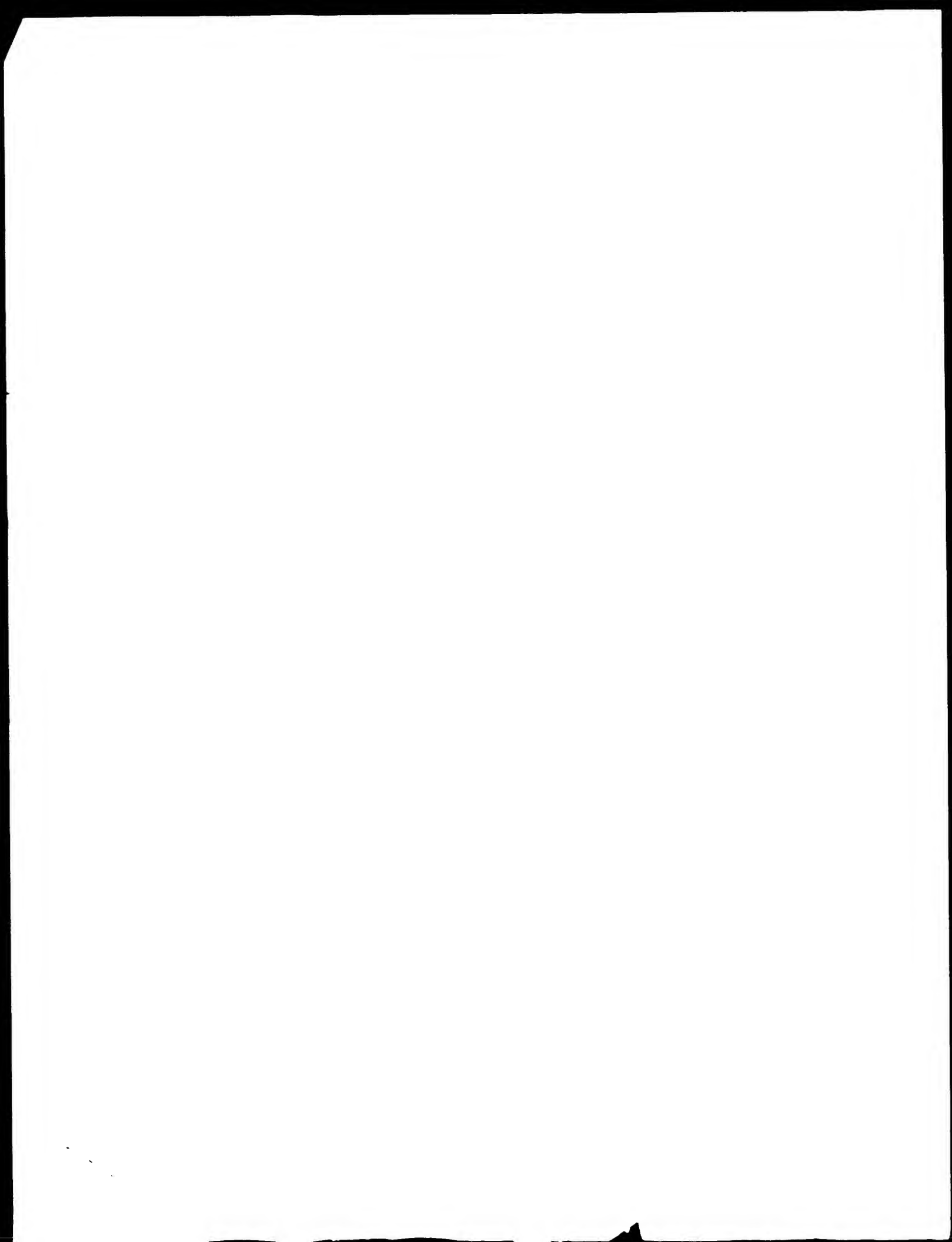
CC APPLICATION NUMBER: US 07/634,278
 CC FILING DATE: 19-DEC-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/590,274
 CC FILING DATE: 28-SEP-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/710,252
 CC FILING DATE: 13-FEB-1989
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/290,975
 CC FILING DATE: 28-DEC-1988
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 11823-002610
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 326-2400
 CC TELEFAX: (415) 326-2422
 CC INFORMATION FOR SEQ ID NO: 72:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 117 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE 117 AA; 12472 MW; 77871 CN;

Query Match 58.3%; Score 543; DB 7; Length 117;
 Best Local Similarity 76.5%; Pred. No. 2.93e-33;
 Matches 75; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

Db 1 QVQLV-QSGAEVKKPGSSVKVSKASGTFSSRAIIWVRQAPGQGLEWMGGIIVPMFGPPN 59
 QY 1 EVQLLEQSGAEVKKPGSSVKVSKCVFGDTFSRYTIQWLRLQAPGGPEWGMNIPVYNTPN 60
 Db 60 YAQKFGQGRVITTADESTNTAYMELSSLRSLEDTAFYFCA 97
 QY 61 YAQKFGQGRVITTADESTNTAYMELSSLRSLEDTAFYFCA 98

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 Job time : 14 secs.

N 95287497 MEDLINE
 DN 95287497
 TI Occurrence of antibodies reactive with more than one variant of the putative envelope glycoprotein (gp70) hypervariable region 1 in viremic hepatitis C virus-infected patients.
 AU Scarselli E; Cerino A; Esposito G; Salini E; Mondelli M U; Triaboni C
 CS Istituto di Ricerche di Biologia Molecolare P. Angeletti (IRBM), Rome, Italy.
 NC A131783 (NIAID)
 P30 A128691 (NIAID)
 P30A06516 (NCI)
 SO JOURNAL OF VIROLOGY, (1995 JUL) 69 (7) 4407-12.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Cancer Journals; Priority Journals
 OS GENBANK-X79671; GENBANK-X79672; GENBANK-X79673
 EM 199509
 AB The hepatitis C virus (HCV) is a frequent cause of chronic liver disease. A mechanism proposed as being responsible for virus persistence is evasion of the host immune response through a high mutation rate in crucial regions of the viral genome. We have sequenced the hypervariable region 1 (HVR1) of the virus isolated from three serum samples, collected during 18 months of follow-up, from an asymptomatic HCV-infected patient. A synthetic peptide of 27 amino acids, corresponding to the HVR1 sequence found to be predominant in both the second and third samples, was used as the antigen for detection of antibodies by enzyme-linked immunosorbent assay (ELISA). We observed reactivity against this HVR1 sequence in the first serum sample before the appearance of the viral isolate in the bloodstream; the reactivity increased in the second and third samples while the cognate viral sequence became predominant. Moreover, our results show that antibodies from all three samples recognize a region mapping at the carboxyl-terminal part of the HVR1 and are cross-reactive with the HVR1 sequence previously found in the same patient. The presence of anti-HVR1 antibodies was investigated in a further 142 HCV patients: 141 viremic and 21 nonviremic. Two synthetic peptides were used, the first corresponding to the sequence derived from the patient described above and the second one synthesized according to the sequence of the HCV BK strain. A high frequency of positive reactions against both HVR1 variants was detected in the samples from the viremic individuals. Finally, antibodies cross-reactive with both variants were shown to be present by competitive ELISA in 6 of 10 viremic patients. The potential negative implications of this observation for the host are discussed.



L2 ANSWER 1 OF 15 MEDLINE
 AN 198229450 MEDLINE
 DN 98229450
 TI Antibodies directed to envelope proteins of hepatitis C virus
 AU Lechner S; Rispeter K; Meisel H; Kraas W; Jung S; Roggendorf M;
 Zibert A
 CS Institut für Virologie, Universitätsklinikum, Essen, Germany.
 SO VIROLOGY, (1993 Apr 10) 213 (2) 313-21.
 Journal code: XEA, ISSN: 0042-6822.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals; Cancer Journals
 EM 199807
 EW 19980705
 AB The relatively high variability of the hepatitis C virus (HCV) envelope proteins E1 and E2 suggests that parts of these proteins other than the hypervariable region 1 (HVR1) might be involved in the induction of virus neutralizing antibodies. To test this hypothesis, two HCV proteins, pE1 and pE2, were generated by in vitro translation. They represent amino acids 174-337 of E1 and 411-668 of E2, respectively, of isolate HCV-AD78; the protein pE2 delta contained no HVR1. As a control, protein pC-HVR1, which represents amino acids 384-410 of HVR1 of isolate HCV-AD78, was expressed separately. These three proteins were used in an immunoprecipitation assay to detect the presence of antiviral antibodies in sera of patients infected with the same isolate of HCV (HCV-AD78). Sera were obtained 4-8 months postinfection from patients who later resolved an acute infection or developed chronic liver disease. A high prevalence of antibodies (up to 35.7%) against pE1 and pE2 delta could be detected in both groups of patients, suggesting that these forms of the HCV envelope proteins contain B-cell epitopes. The antibody responses against proteins pE1 and pE2 delta did not differ significantly between patients with resolving or chronic infection, whereas antibodies against protein pC-HVR1 were associated with resolution of infection. Rabbit antisera raised against pE1 and pE2 delta were tested for their ability to neutralize the binding of HCV to susceptible cells in tissue cultures. The results suggested that although a few B-cell epitopes outside of HVR1 can induce virus neutralizing antibodies, these antibodies are probably not associated with the resolution of infection.

L2 ANSWER 3 OF 15 MEDLINE
 AN 1998010011 MEDLINE
 DN 98010011
 TI Characterization of antibody response to hepatitis C virus protein E2 and significance of hypervariable region 1-specific antibodies in viral neutralization.
 AU Zibert A; Dudziak S; Schreier E; Roggendorf M
 CS Institut für Virologie, Universitätsklinikum Essen, Federal Republic of Germany.
 SO ARCHIVES OF VIROLOGY, 1997; 142 (3) 523-34.
 Journal code: 8L7, ISSN: 0304-8568.
 CY Austria
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English



Antibodies directed against hypervariable region 1 (HVR1) of hepatitis C virus (HCV) have recently been shown to neutralize the corresponding HCV isolate *in vitro*. We analyzed the appearance of antibodies directed to HVR1 during the course of infection in a large group of patients who have been infected by the same isolate of a HCV contaminated anti-D immunoglobulin (HCV-AD78). An enzyme-linked immunosorbent assay (ELISA) was established using a synthetic peptide to detect antibodies against the main HVR1 variant of HCV-AD78. 107 sera obtained at different time points post infection (p.i.) of 51 patients having either acute self-limiting (n = 28) or chronic infection (n = 79) were studied. Antibodies directed to HVR1 were found at least at one time point during the infection course in 15 of 28 patients (53%) having acute self-limiting infection and in 17 of 79 patients (74%) with chronic disease. The time of appearance of anti-HVR1 was significantly different between these two patient groups (p = .025) although appearance and titers of other HCV-specific antibodies were found to be similar at early time points p.i. In acute self-limiting infections 9 of 28 sera (32%) of respective patients with sera available within the first 6 months p.i. were anti-HVR1 positive. The highest prevalence of anti-HVR1 in this group of patients was within month 6 to 12 p.i. (64%). None of the sera available after 24 months p.i. had such antibodies. In contrast, only 2 of 15 sera (13%) of chronically infected patients with respective time points of sera were anti-HVR1 positive within the first 6 months p.i. and only 5 of 13 sera (38%) were positive within month 7 to 12 p.i. Seven patients with chronic HCV infections showed at least two consecutive anti-HVR1 negative early time points up to month 18 p.i. Prevalence of anti-HVR1 after 24 months p.i. was high (84%) in this group of patients and most of the patients

Antibodies directed against hypervariable region 1 (HVR1) within the viral glycoprotein E2 of hepatitis C virus (HCV) are postulated to neutralize virus. An *in vitro* infection/binding assay of human fibroblast cells was established in order to study neutralization of HCV, occurrence of mutations in the nucleotide sequence of HVR1 as compared to the inoculum after infection of human fibroblasts suggested replication of HCV in these cells. The significance of HVR1-specific antibodies in sera of patients who were infected in a single-source outbreak by an HCV contaminated anti-D immunoglobulin (IgG) preparation was studied. Using immunoprecipitation and ELISA, HVR1-specific antibodies could be detected in most of the sera obtained early (< or = 1 year p.i.) and late (up to 14 years p.i.) in single patients. Further characterization of the HVR1-specific antibodies in patient sera by attachment studies of HCV to the human fibroblasts suggested that HVR1-specific antibodies in sera obtained early p.i. can neutralize virus of the anti-D IgG preparation.

ANSWER 4 OF 15 MEDLINE
 97286278 MEDLINE
 97286278
 Early antibody response against hypervariable region 1 is associated with acute self-limiting infections of hepatitis C virus.
 AU Zibert A; Meisel H; Kraas W; Schulz A; Jung G; Roggendorf M
 CS Institut für Virologie, Universitätsklinikum Essen, Germany.
 SO HEPATOLOGY, (1997 May) 25 (5) 1245-9.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199707
 EW 19970705
 AB



maintained high levels of anti-HVRI for up to 17 years p.i. Our findings suggest clearance of virus by respective neutralizing antibodies resulting in a self-limiting infection and may have implications for prognosis of the disease and also for any future vaccine development.

Epitope mapping of antibodies directed against hypervariable region 1 in acute self-limiting and chronic infections due to hepatitis C virus.

Zibert A; Kraas W; Meisel H; Jung G; Roggendorf M
 Institut für Virologie, Universitätsklinikum Essen, Germany.
 JOURNAL OF VIROLOGY, (1997 May) 71 (5) 4123-7.
 Journal code: JCV, ISSN: 0022-538X.

United States
 Journal: Article; (JOURNAL ARTICLE)
 English
 Priority Journals: Cancer Journals
 EM 199707
 EW 19970701

Epitopes of hypervariable region 1 (HVRI) were mapped by enzyme-linked immunosorbent assay using follow-up sera of patients, all of whom were infected with the same isolate of hepatitis C virus (HCV). Our results suggest that (i) an early appearance (up to month 13 postinfection) of antibodies directed to the N terminus of HVRI is associated with acute self-limiting infections of HCV and (ii) isolate-independent antibodies which are mainly directed to the C terminus of HVRI seem to persist in chronically infected patients. The relevance of HVRI-specific antibodies for neutralization was evaluated by characterization of a rabbit serum.

=> d bib,ak 6

LC ANSWER 5 OF 15 MEDLINE
 AN 97048466 MEDLINE
 DN 97048466
 TI Epitope mapping of antibodies directed against hypervariable region 1 of hepatitis C virus can block viral attachment.

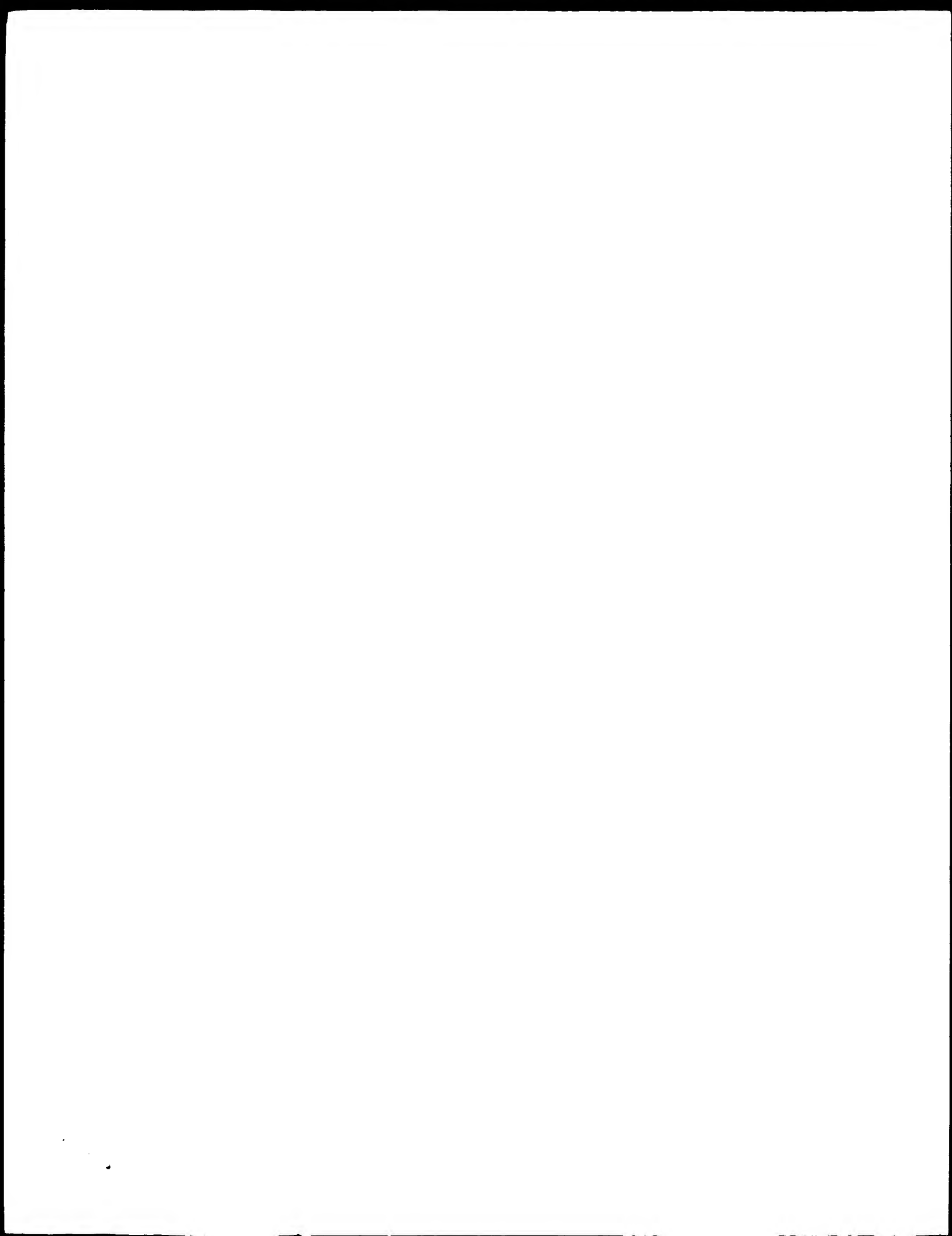
Zibert A; Schreier E; Roggendorf M
 Institute of Virology, University of Essen, Germany.
 VIROLOGY, (1995 Apr 20) 208 (2) 653-61.
 Journal code: JEA, ISSN: 0092-6822.

United States
 Journal: Article; (JOURNAL ARTICLE)
 English
 Priority Journals: Cancer Journals
 EM 199503
 AB It has been postulated that antibodies specific to the hypervariable region 1 (HVRI) within the putative envelop protein E2 of hepatitis C virus (HCV) can neutralize virus. We studied such antibodies in sera of patients who were infected in a single-source outbreak by a contaminated anti-D immunoglobulin preparation (HCV-AD78). The nucleotide sequences of cDNAs encoding HVRI of HCV-AD78 were determined. The four major variants (HVRI-A, B, C, and D) were expressed as fusion proteins in Escherichia coli. Sixty-seven percent of sera contained antibodies to HVRI-A. Sera unrelated to infection of the outbreak also recognized HVRI-A but to a lesser extent (13%), suggesting that not all HVRI-specific antibodies are absolutely isolate-specific. Antibodies directed against individual variants of HVRI were found in sera obtained early postinfection (p.i.) (< or = 1 year) but also in sera obtained several years later. An in vitro binding assay of HCV to tissue culture cells was

LC ANSWER 5 OF 15 MEDLINE
 AN 97048466 MEDLINE
 DN 97048466
 TI Epitope mapping of antibodies directed against hypervariable region 1 in acute self-limiting and chronic infections due to hepatitis C virus.

Zibert A; Kraas W; Meisel H; Jung G; Roggendorf M
 Institut für Virologie, Universitätsklinikum Essen, Germany.
 JOURNAL OF VIROLOGY, (1997 May) 71 (5) 4123-7.
 Journal code: JCV, ISSN: 0022-538X.

United States
 Journal: Article; (JOURNAL ARTICLE)
 English
 Priority Journals: Cancer Journals
 EM 199707
 EW 19970701



employed to further characterize these sera. Five of seven sera that were obtained early p.i. prevented binding of HCV to cells. Preincubation of such sera with HVR1-specific fusion proteins restored binding of HCV to cells in four of five sera. These findings suggest that the majority of neutralizing antibodies are directed against HVR1.



WATERL

(TM)

Release 2.12 John F. Collins, Biocomputing Research Unit
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Distribution rights by IntelliGenetics, Inc.

MPSrch_n n.a. - n.a. database search, using Smith-Waterman algorithm
Feb 26 7:04 Feb 24 07:22:45 1998 MasPar time 50.94 seconds
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Gap 6

Nmatch STD : Dbase 0; Query 0
Searched: 159551 seqs, 57698962 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

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8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
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Statistics: Mean 8.010; Variance 4.828; scale 1.659
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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7	244	78.2	1204	2	Q11879	1204	2	Q11879	1204	2	Q11879	IgG light chain varia	5.71e-148	5.71e-148	5.71e-148	5.71e-148	5.71e-148
8	244	78.2	1204	2	Q11879	1204	2	Q11879	1204	2	Q11879	IgG light chain varia	5.71e-148	5.71e-148	5.71e-148	5.71e-148	5.71e-148
9	232	74.4	1011	2	Q11879	1011	2	Q11879	1011	2	Q11879	Anti-pseudomonas aer	1.36e-139	1.36e-139	1.36e-139	1.36e-139	1.36e-139
10	232	74.4	1011	2	Q11879	1011	2	Q11879	1011	2	Q11879	Anti-pseudomonas aer	1.36e-139	1.36e-139	1.36e-139	1.36e-139	1.36e-139
11	230	73.7	4691	16	Q22546	4691	16	Q22546	4691	16	Q22546	pComb3 expression vec	3.38e-138	3.38e-138	3.38e-138	3.38e-138	3.38e-138
12	230	73.7	4691	16	Q22546	4691	16	Q22546	4691	16	Q22546	pComb3 expression vec	3.38e-138	3.38e-138	3.38e-138	3.38e-138	3.38e-138
13	228	73.1	646	12	Q20487	646	12	Q20487	646	12	Q20487	Expression vector, pp	8.38e-137	8.38e-137	8.38e-137	8.38e-137	8.38e-137
14	228	73.1	646	12	Q20487	646	12	Q20487	646	12	Q20487	Anti-tetanus toxoid 1	8.38e-137	8.38e-137	8.38e-137	8.38e-137	8.38e-137
15	226	72.4	924	10	Q11879	924	10	Q11879	924	10	Q11879	Sequence coding human	2.08e-135	2.08e-135	2.08e-135	2.08e-135	2.08e-135

16	218	62.9	900	7	Q41234	900	7	Q41234	900	7	Q41234	Human DNA fragment vk	7.75e-130
17	218	62.9	900	12	Q78854	900	12	Q78854	900	12	Q78854	Human V-kappa gene vk	7.75e-130
18	218	62.9	900	27	737180	900	27	737180	900	27	737180	DNA fragment vk65.3	7.75e-130
19	215	59.2	390	7	Q42707	390	7	Q42707	390	7	Q42707	Immunoglobulin F105VK-F105JK	7.91e-128
20	214	58.6	372	32	739922	372	32	739922	372	32	739922	Immunoglobulin F105	4.71e-127
21	214	58.6	387	7	Q42155	387	7	Q42155	387	7	Q42155	F105 rearranged varia	4.71e-127
22	213	68.3	390	7	Q42706	390	7	Q42706	390	7	Q42706	vk325-1k2	2.34e-125
23	212	67.9	324	5	Q29766	324	5	Q29766	324	5	Q29766	Gene for Lx region of	1.16e-125
24	208	60.7	345	25	144941	345	25	144941	345	25	144941	Fluorimetric analysis of	5.80e-123
25	206	66.0	325	11	Q65538	325	11	Q65538	325	11	Q65538	Light chain of Ambal	1.71e-121
26	206	66.0	402	28	733664	402	28	733664	402	28	733664	Anti-lung tumour anti	1.71e-121
27	201	64.4	642	25	744090	642	25	744090	642	25	744090	Ulcerative colitis-as	5.08e-118
28	179	57.4	416	31	149345	416	31	149345	416	31	149345	cDNA encoding kappa-l	9.72e-103
29	158	53.8	338	29	759131	338	29	759131	338	29	759131	Coding sequence for i	3.38e-95
30	165	52.9	324	16	Q92549	324	16	Q92549	324	16	Q92549	PM24-3 fragment enco	3.93e-93
31	162	51.9	729	24	140913	729	24	140913	729	24	140913	DNA encoding modified	4.55e-91
32	162	51.9	13254	24	140915	13254	24	140915	13254	24	140915	Nucleotide sequence o	4.55e-91
33	156	50.0	341	28	760119	341	28	760119	341	28	760119	Coding sequence for i	6.01e-87
34	149	47.8	390	14	Q87237	390	14	Q87237	390	14	Q87237	Anti-interleukin-1 al	3.80e-82
35	149	47.8	496	7	Q42345	496	7	Q42345	496	7	Q42345	h1229 Ab i chain V re	2.89e-82
36	148	47.4	437	29	742622	437	29	742622	437	29	742622	Light chain transcript	1.84e-81
37	147	47.1	702	7	Q43773	702	7	Q43773	702	7	Q43773	Sequence encoding the	8.90e-81
38	145	46.8	381	11	Q84167	381	11	Q84167	381	11	Q84167	Sequence of mouse V-k	4.30e-80
39	145	46.5	324	33	772135	324	33	772135	324	33	772135	CEA-specific antibody	2.08e-79
40	145	46.5	396	31	775423	396	31	775423	396	31	775423	Human anti-tumour ant	2.08e-79
41	144	46.2	324	33	760371	324	33	760371	324	33	760371	Anti-TGF beta-2 scFv	1.00e-78
42	144	45.2	341	28	760117	341	28	760117	341	28	760117	Coding sequence for i	1.00e-78
43	143	45.8	366	32	779921	366	32	779921	366	32	779921	Immunoglobulin F6B7	4.84e-78
44	143	45.8	645	13	Q67894	645	13	Q67894	645	13	Q67894	cDNA contg an ORF fo	4.84e-78
45	142	45.5	285	14	Q89324	285	14	Q89324	285	14	Q89324	S43434 VK-1 gene.	2.33e-77

ALIGNMENTS

RESULT 1
ID T37180 standard; DNA: 812 BP.
AC T37180;
DE 14-APR-1997 (first entry)
DE DNA fragment vk65.3, containing variable kappa chain gene.
KW Variable: kappa chain; gene segment; human; DNA fragment: vk65.3;
KW unrearranged, light chain; minilocus; transgene; transgenic; mouse;
KW production; heterologous; antibody; gamma; immunoglobulin, ss.
QS Homo sapiens.
FH Key Location/Qualifiers
FT exon 199..247
FT /*tag= a 419..717
FT /*tag= b
FT /*tag= b
PN US5545806-A.
PD 13-AUG-1996.
PR 29-AUG-1990; 574748.
PR 31-AUG-1990; US-574748.
PR 29-AUG-1990; US-575962.
PR 17-DEC-1991; US-810279.
PR 18-MAR-1992; US-853408.
PR 23-JUN-1992; US-904068.
PR 16-DEC-1992; US-990860.
PA (GENP-) GENPHARM INT INC.
FI Kay RM, Tomberg N,
DR WPI, 96-383736/38.
DR P-FSDB: W03946.
FI Prodn of heterologous human immunoglobulin(s) - by immunising
PT Transgenic mice
PS Example 21, Fig 41, 94pp, English.
CC The present sequence is the variable kappa chain gene segment
CC containing human DNA fragments vk65.3, which was co-injected along
CC with the human DNA fragments vk65.5, vk65.8 and vk65.15 into half
CC day mouse embryo pronuclei, to generate an unrearranged light chain
CC minilocus transgene. The resulting transgenic mice can be used for
CC the production of heterologous (i.e. human) antibodies against
CC specific antigens, this comprises immunising a mouse with a
CC preselected antigen and collecting antigen binding heterologous
CC human gamma immunoglobulins.

QY	67	GCAGTCAGAGTGTTA--A-CAAGTACTT	AGCTGGTACCAACAGAAACTGGTCAGGCT	123
Db	704	cccaggtcctcatctatctgcgtccagcaggccactggcatccacagaggttcagt	763	
QY	124	CCCAGGCTCCCTCATCTATGATGCATCCAAACAGGCGCCACTGGCATCCAGCCAGGTTCA	183	
Db	764	ggcagtggtctggggcagaactctcactctcaccatcagtagatgagaaacctgaagattct	823	
QY	184	GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAACCTAGAGCTCAAGATTTT	243	
Db	824	gcaatgattactgtcagcagtagcacgcctctgcatccttcctggcgaggagaccgaattg	883	
QY	244	GCAGTTTATTACTGTCAGCAGCGTAGCAGCTGGGTCACTTTCGGCGAGGGACCAAGG	303	
Db	884	gacatcaaa	892	
QY	304	GAGATCAAA	312	

RESULT 10
 ID N91359 standard; DNA: 1011 BP.
 AC N91359.
 DE 02-WAR-1990 (first entry)
 DT Anti-P. aeruginosa strain F4 light chain V and J coding regions
 KW Immunoglobulin.
 OS Pseudomonas aeruginosa F4.
 Key Location/Qualifiers
 FT CDS 325..372
 FT /*tag= a 560..895
 FT /*tag= b 264..271
 FT /*tag= c
 PN J01211498-A.
 PD 24-ADG-1986.
 PF 19-FEB-1988; 035395.
 PR 19-FEB-1988; JP-035395.
 RA (WAKU) Wakumaga Seliyaku KK.
 DR WPI: 89-303485/42.
 DR P-PSDB: P91001
 PT Production of human IgG monoclonal antibody - by converting human
 PT antibody into other subclasses by genetic engineering
 PS Disclosure: fig. 3; 17pp; Japanese
 CC This encodes a variable chain and can be connected to a gene encoding
 CC a constant region which determines optional IgG subclass. This can be
 CC used to study subclasses, and as an antigen for prep. IgG1 or IgG3
 CC antibody. Regions 325-372 connected to 560-571 encode the L chain.
 CC region 572-856 encodes V chain and region 857-895 encodes J chain.
 SQ Sequence 1011 BP; 237 A; 263 C; 254 G; 257 T;

Query Match	74.4%	Score 232;	DB 1;	Length 1011;
Best Local Similarity	90.0%	Pred No. 1.36e-139;		
Matches	Local 278;	Conservative 0;	Mismatches 28;	Indels 3; Gaps 27;

Db	584	acgcagtcctcagggaccctctgtttgtctccagggggaagaccacctctctcaggg	643
QY	7	ACTCAGTCCAGCCAGCCCTGTCTTGTCTCAGTGGGAAAGACCCACTCTCTCTCAGG	66
Db	644	gccagtcagagtattagcagcaatccttagcctggtaccacagaaacctggccaggt	703
QY	67	GCACGTCCAGATGTGTA--A-CAAGTACTTAGCCTGGTACCAACAGAAACTGGCCAGGCT	123
Db	704	cccaggtcctcatctatgctggtccagcaggccactggcatccacagaggttcagt	763
QY	124	CCCAGGCTCCCTCATCTATGATGCATCCAAACAGGCGCCACTGGCATCCAGCCAGGTTCA	183
Db	764	ggcagtggtctggggcagaactctcactctcaccatcagtagatgagaaacctgaagattct	823
QY	184	GGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAACCTAGAGCTCAAGATTTT	243
Db	824	gcaatgattactgtcagcagtagcacgcctctgcatccttcctggcgaggagaccgaattg	883
QY	244	GCAGTTTATTACTGTCAGCAGCGTAGCAGCTGGGTCACTTTCGGCGAGGGACCAAGG	303

884 gacatcaaa 892
 ||| |||||
 304 GAGATCAAA 312

RESULT 11
 ID Q92546 standard; DNA; 4691 BP.
 AC 192546;
 DT 11-MAR-1996 (first entry)
 DE pComb3 expression vector.
 CC pComb3; phagemid expression phase; bacteriophage; coat protein 3;
 CC Gene 11; filamentous phase; minor phage coat protein; cp11; cp3;
 CC KW bacterial membrane; periplasm; E. coli; human; Fab, HIV, gp120;
 CC KW recombinatorial Fab library; cassette; Fd/cp3; lacZ promoter/operator;
 CC KW ribosome binding site; RBS; PelB leader; spacer; tether sequence;
 CC MT4; pMT4-3; antibody; ss; cyclic.
 CC KW Synthetic.
 CC OS WO9511317-A1.
 CC PN 27-APR-1995.
 CC PD 19-OCT-1994; U11907.
 CC PF 19-OCT-1993; US-139409.
 CC PR 26-APR-1994; US-233619.
 CC PR 19-SEP-1994; US-308841.
 CC PA (SCRI) SCRIPPS RES INST.
 CC PI Barbas CF, Burton DR, Lerner RA;
 CC WP1, 95-170235/22.
 CC PT Synthetic human neutralising monoclonal antibodies to human
 CC PT Immunodeficiency virus - used for diagnosis and immuno:therapy of
 CC PT HIV-induced disease
 CC PS Example 1; Page 185-188; 249pp; English.
 CC This sequence represents the pComb3 phagemid expression vector. This
 CC vector has been designed to allow for anchoring of expressed proteins on
 CC the bacteriophage coat protein 3. Gene 11 of filamentous phase encodes
 CC the 406 residue minor phage coat protein, cp11 (cp3), which is expressed
 CC prior to extrusion in the phase assembly process on a bacterial membrane
 CC and accumulates on the inner membrane facing into the periplasm of E.
 CC coli. This plasmid was used within the scope of the invention to express
 CC various mutagenised human Fab's which comprise heavy and light variable
 CC regions which bind to HIV gp120. pComb3 allows for both surface display
 CC and soluble forms of the Fabs. The vector consists of a DNA molecule having
 CC of combinatorial Fab libraries. pComb3 consists of a 3' XbaI restriction site
 CC two cassettes to express one fusion protein, Fd/cp3, and one soluble
 CC protein, the light chain. The finished vector comprises, operatively
 CC linked 5' to 3', a first cassette consisting of lacZ promoter/operator
 CC sequences, a NotI restriction site, a cloning region bordered by 5' XbaI and
 CC 3' SpeI restriction sites, the tether sequence, the sequences encoding
 CC bacteriophage cp3 followed by a stop codon, a PelB leader, a spacer region, a
 CC between the two cassettes, and a second lacZ promoter/operator sequence,
 CC followed by an expression control RBS, a 3' XbaI restriction site,
 CC cloning region bordered by 5' SacI and 3' XbaI restriction sites,
 CC followed by expression control stop sequences and a second NotI
 CC restriction site. The pComb3 expression vector forms the basic construct
 CC of the M74 Fab display phagemid expression vector, pMT4-3 (see also
 CC Q92540), used in the invention for the production of synthetic human Fab
 CC antibodies against gp120 of HIV.
 CC Sequence 4691 BP: 1176 A: 1171 C: 1232 G: 1118 T:
 CC

Query Match 73.78; Score 230; DB 16; Length 4691;
 Best Local Similarity 88.94; Pred. No. 3,38e-138;
 Matches 289; Conservative 0; Mismatches 32; Indels 4; Gaps 1;

Db 2677 gagctcagcagctctccagcaccctctcttctctccagggaaagaaagcactctctcc 2736
 QY : GAATCTATCTCCAGCACGCTGCTGTTGTCCTACGAGAAAGACGACCTCTCC 60

Db 2737 tacagggccagctcacagctgttagcaggcctacttagcttgatctatccagcgaacactagc 2796
 QY : TCCAGGCGGCGCTCAGACAGTGTAAAG---TACTTAGCTGTGTACCAACAGAGAACTGGC 117

Db 2797 cagggtccccagcctcctcatctatgattacatccagcaggcactagcatccagacacg 2856
 QY : TCCAGGCGGCGCTCAGACAGTGTAAAG---TACTTAGCTGTGTACCAACAGAGAACTGGC 117

181	tccaatgacgaatggtctcaggacaaacttcactctcaccatcagcagactgagacctgaa	240
Db		
178	TTCAGTGGCAGTGGGTCTGGACAGACTTCCTACCTCACCATCAGCAACCTAGAGCTGAA	237
Qy		
241	gatttcgagtgactactctcagcagatggtgtggtctcgcgcaaggacc	300
Db		
238	GATTTTCAGTTATTACTGTCAGCAGCGTAGGACTGGGTCTACTTTTCGCGAGGGGACC	297
Qy		
301	aaggtggaactcaaa	315
Db		
298	AAGGTGGAGATCAAA	312
Qy		

RESULT 14
 ID T15203 standard; CDNA: 646 BP.
 AC T15203:
 DE 23-OCT-1996 (first entry)
 DE PC3AP13 anti-tetanus toxoid Ig light chain variable domain cDNA.
 DE Mutagenesis; Ig; immunoglobulin; FR; framework region; variable; CDR;
 KW complementarity determining region; light; heavy chain; PCR;
 KW polymerase chain reaction; antibody library; diversity; affinity;
 KW immunospecificity; ss.
 OS Synthetic.
 OS WO9607754-A1.
 PN 14-MAR-1996.
 PD 01-SEP-1995; U11235.
 PF 02-SEP-1994; US-300386.
 PI (SCRI) SCRIPPS RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 PI WPI, 96-171525/17.
 DR Oligo-nucleotide(s) for inducing mutagenesis in an Ig light chain
 PT gene CDR - useful for prodn. of Ig heavy and light chain
 PT combinatorial antibody libraries
 PT Example 1; Page 84; 125pp; English.
 PS T15202 and T15203 are the heavy and light chain variable domains of
 PS a human anti-tetanus toxoid immunoglobulin (Ig) encoded by a Pcomb3
 PS based expression vector. The heavy and light chain variable domains
 PS are used in an example to demonstrate the prodn. of antibodies for
 PS an antibody library using mutagenic primers. Mutagenic primers of the
 PS invention have sequences at their 3' and 5' ends both capable of
 PS binding different framework regions linked by a sequence 6 to 50
 PS nucleotides long. Different immunoglobulins produced using the
 PS primers may be used to produce antibody libraries having diverse and
 PS novel immunospecificities and affinities. By using mutagenic ONS an
 PS extremely large population of different randomised binding sites can
 PS be created and use of the universal light chain increases the number
 PS of combinations which yield functional heterodimeric antibodies
 PS Sequence 646 BP; 162 A; 187 C; 170 G; 127 T.

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Query Match      73.1%, Score 428, DB 22, Length 646;
Best Local Similarity 88.6%;
Matches 279, Conservative 0; Mismatches 33; Indels 3; Gaps 1;

1 gacgtcacgcagctctccaggcacacctgtttgtctccaggggaaagagccacctctcc 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 GAGCTCACTCAGTCTCCAGGCCACCGTCTTTCTCTCCAGGGGAAAGAGCCACCTCTCC 60

      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 tccaggccagtcacaggtttagcaggggctacttgaacctgtaccagcaaaactggc 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
c1 tccagggccagctcagactcagactttaaag--TACTTAGGCTGGTACCAACAGAAACCTGGC 117

      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
121 caggctccccaggctctctctatctatgtgtatcatccagcagagccactggcatcccaagcag 180

      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
118 CAGGCTGCCAGGCTCTCTATCTATCATGCATCCCAAGAGGCCACCTGGCATCCCAGCCAG 177

      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
181 tccagtgagcagtggtgtctgggacagacttcactctaccatcagcagactggaccttgaa 240

      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
178 TTCAGTCCCAAGTGGGTGTGGACAGACTTTCACTCTCACCATCAGCAACCTAGAGCCTGAA 237

      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
241 gatttcagtgatactactgcagcagatgatggtggctcacctgtgtctggcccaaggacc 300

      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
238 GATTTCGAGTTTATTACTCTCAGCAGGCTACCGACTGGGTCACTTTCGGCGGAGGGAGCC 297

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301 aagdtggaactcaaa 315
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298 AAGGTGGAGATCAA 312

RESULT 15
ID Q71872 standard; cDNA; 924 BP.
AC Q71872;
DT 27-OCT-1994 (first entry)
DE Sequence coding human anti-IgE MAB light chain.
ID Human IgE; CH4 region; triggers mediator release;
KW Mast cells; Monoclonal antibody; allergy; Immunoglobulin; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT misc_feature 4..6
FT /*tag= d
FT /note= "C or G, illegible sequence."
FT misc_feature 908..910
FT /*tag= b
FT /note= "N is an unidentified base"
FT misc_feature 71..394
FT /*tag= c
FT /note= "L-chain variable region"
FT CDS 11..715
FT /*tag= d
FT /product= antibody light chain
FT /note= "Human monoclonal anti-IgE antibody "
FT EP 592230-A.
FT 13-APR-1994.
PD 07-OCT-1993; 308006.
PR 07-OCT-1992; JP-293800.
PA (SNOW ) SNOW BRAND MIK PROD CO LTD.
PI Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;
PI Yoshida T;
PI WFI; 94-120330/15.
DR P-PSDB; K52951.
DR Human monoclonal anti-IgE peptide antibody - inhibits histamine
PT release from mast cells by allergen stimulation, useful for
PT preventing allergies
PS Claim 4; Page 17; 21pp; English.
CC Q71872 encodes the light chain of a human type anti-IgE peptide
CC monoclonal antibody which inhibits the signal transduction for
CC the release of chemical mediator from mast cells and basophils
CC stimulated with allergen. The antibody can be used for the
CC prophylaxis and the therapy of allergy.
CC Sequence 324 BP, 298 A, 277 C, 216 G, 195 T;
SQ

Query Match 72.4%; Score 226; DB 10; Length 924;
Best Local Similarity 89.0%; Pred. NO. 2,08e-115;
Matches 275; Conservative 0; Mismatches 31; Indels 4; Gaps

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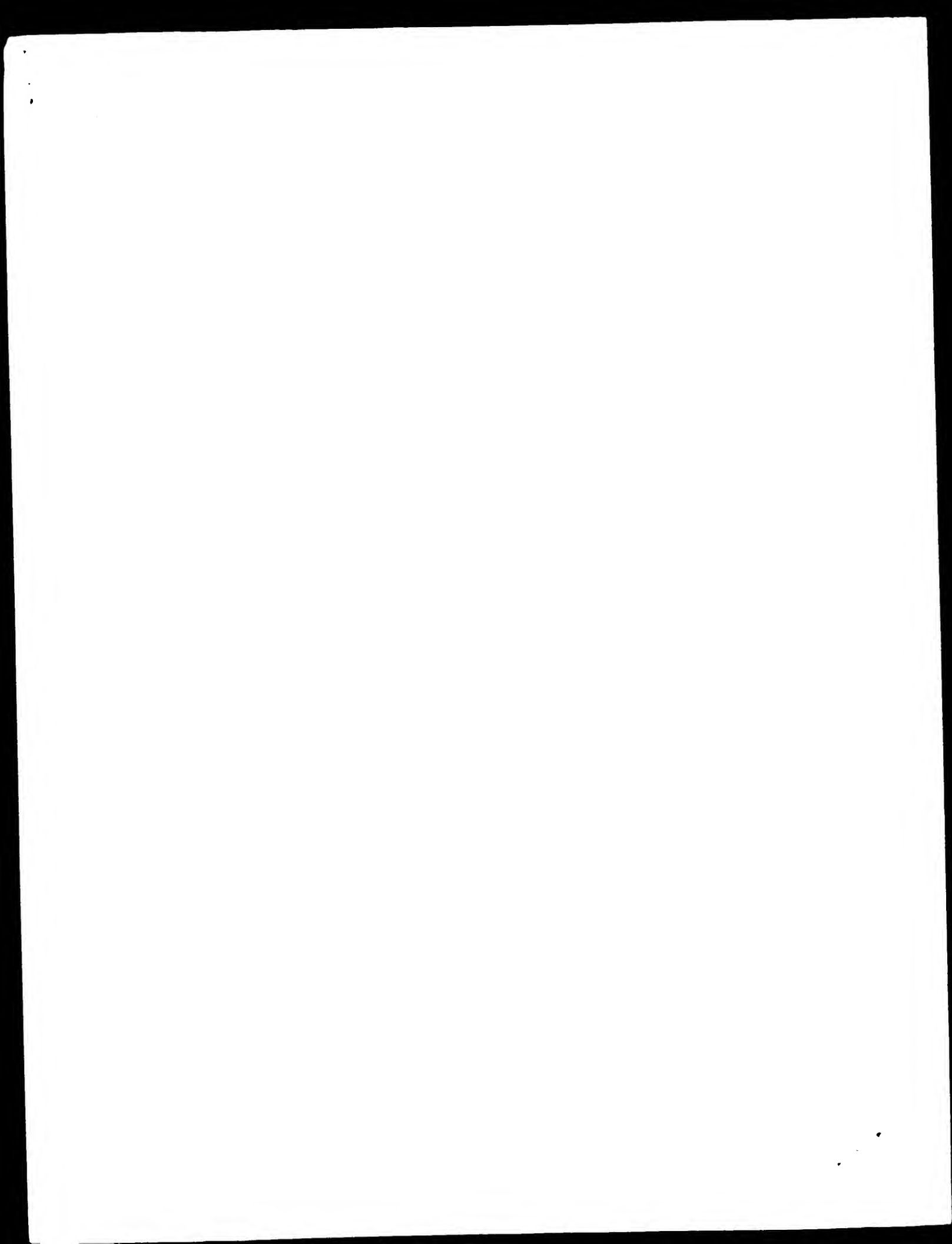
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Page 9

11 11111
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REFERENCE 1 (bases 1 to 823)
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubouque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, L., Lennon, S., Soares, B., Wilson, K. and Waterston, K.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLM: contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:379418
 Putative full length read
 vector to vector length is 867
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 492

FEATURES
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 /strain="C57BL/6J"
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 /clone="618594"
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 /tissue_type="Spleen"
 /dev_stage="4 weeks"
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 ORIGIN

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 Matches 183; Conservative 0; Mismatches 104; Indels 2; Gaps 2.
 Db 118 qacgtgaagctgtgagctctgggaaggcttagtaagcctgagaggtccctgaacac 177
 QY 1 CAGGTGCAGCTGCTGCAATTTGGGTCAGAGTGAAGAGCTTGGGTCCTTGGGTCAGAGGTC 60
 Db 178 tccgtgacgctctgagctaccttccagtagctatgccatgtctgggttcgccagact 237
 QY 61 TCCTGCAGGGCCTCTGGAGGCAGCTTCAGAAGCTTACAATTTCAATTGGGTGGCAGAGGCC 120
 Db 238 ccagaagaagagctgaggtgggtgcacattagtagtagtgatgattacatcta-cta 296
 QY 121 CCTGGACAGAGTCTGAGTGGATGGAGGATCATCCCTA-TGTTGGGAACACCAACTA 174
 Db 297 tgcagacactgtgaagggccgattccaccattccagagacaatgccaggaacacctgta 356
 QY 180 GGCACAGAAATTTTCAGGGCAGAGTCACAAATATCTGGAGACCAATCCAGCCACAGGCTA 234
 Db 357 cctccaatagcagctgtgaagctgtgaggacacagccatattactgt 405
 QY 240 CATGGATTGACGAGTGTGATGATGGAAGACAGAGGCGGTTTATTACTGT 288
 RESULT 6

LOCUS SSC1D10 330 bp RNA EST 03-SEP-1996
 DEFINITION S. scrofa mRNA: expressed sequence tag (5' clone c1410).
 ACCESSION F14516
 NID 971726
 KEYWORDS diversity region; EST: expressed sequence tag; immunoglobulin; immunoglobulin heavy chain; joining region; variable region.
 SOURCE pig
 ORGANISM Sus scrofa
 Eukaryotes; mitochondrial eukaryotes Metazoa; Chordata; Vertebrata; Eutheria; Artiodactyla; Suiformes; Suina; Suidae; Sus.
 REFERENCE 1 (bases 1 to 330)
 AUTHORS Winteroe, A. K., Fredholm, M. and Davies, W.
 TITLE Evaluation and characterization of a porcine small intestine cDNA library
 JOURNAL Mamm. Genome 7, 509-517 (1996)
 REFERENCE 2 (bases 1 to 330)
 AUTHORS Winteroe, A. K.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUL-1995) Winteroe A. K., The Royal Veterinary and Agricultural University, Department of Animal Science and Animal Health, Division of Animal Genetics, Bulowsovej 13, 1870 Frederiksberg C, DENMARK
 FEATURES
 Location/Qualifiers
 source 1..330
 /organism="Sus scrofa"
 /tissue_type="small intestine"
 /clone_lib="directionally cloned cDNA in X11-blue MRF"
 /clone="cid10"
 1...>330
 /note="expressed sequence tag"
 /product="Ig heavy chain variable VDJ region"
 BASE COUNT 71 a 77 c 104 g 76 t 2 others
 ORIGIN

Query Match 16.7%; Score 63; DB 123; Length 330;
 Best Local Similarity 61.2%; Pred. No. 2.74e-76;
 Matches 167; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
 Db 58 gagagaagagtggtgagctctgagggagggcctggtgagctgagaggtctctgaacac 117
 QY 1 CAGGTGCAGCTGCTGCAATTTGGGTCAGAGTGAAGAGCTTGGGTCCTTGGGTCAGAGGTC 60
 Db 118 tccgtgacgctctgagctaccttccagtagctatgccatgtctgggttcgccagact 177
 QY 61 TCCTGCAGGGCCTCTGGAGGCAGCTTCAGAAGCTTACAATTTCAATTGGGTGGCAGAGGCC 120
 Db 178 ccaggaagaagagctgaggtgggtgcacattagtagtagtgatgattacatcta-cta 247
 QY 121 CCTGGACAGAGTCTGAGTGGATGGAGGATCATCCCTA-TGTTGGGAACACCAACTA 180
 Db 238 ccaggaagctgaggaagagctctccaccattccagagacaatgccaggaacacctgta 297
 QY 181 GTCAGAAATTTTCAGGGCAGAGTCACAAATATCTGGAGACCAATCCAGCCACAGGCTA 240
 Db 298 ctggaataaagacagctgaggaagaagacacacacacacacacacacacacacacacac 330
 QY 241 ATGGAGTTCAGACACTCTGAGATCTGAGATCTGAGATCTGAGATCTGAGATCTGAGATCT 273
 RESULT 7
 LOCUS H73816 419 bp mRNA EST 41-OCT-1995
 DEFINITION IG Heavy Chain V-111 REGION (HUMAN).
 ACCESSION H73816
 NID g1046750
 KEYWORDS EST.
 SOURCE human clone-214441 primer-M13R1 library-Soares total liver spleen
 INFLS vector-pT73D (Pharmacia) with a modified polylinker
 host=DH10B (ampicillin resistant) Ksile-Pac 1 Ksile-Pac 1 Ksile-Pac 1 Ksile-Pac 1
 and spleen from a 20 week-old fetus of a 20 week-old fetus 1st strand
 cDNA was primed with a Pac 1 - oligo(dT) primer [5',
 AACTGGAAGAAATTAATTAAGATCTTTTTTTTTTTTTTTT 3']. double-stranded
 cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac

and M Fatima Ronaldo.
Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Saurpteryalia; Chelonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 97)
Hillier, L., Clark, N., Dubouque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, C., Merritt, M.,
Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, P.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson PK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8001, St. Louis, MO 63110
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL. Contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality.
Location/Qualifiers

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Query Match      11.9%; Score 45; DA 64; Length 47;
Best Local Similarity 68.0%;
Matches          66; Conservative 41; Indels 0; Gaps 0;
BASE COUNT      25 a 23 c 21 g 18 t 10 others
ORIGIN
197
/oranism="Hom sapiens"
/clone="188012"

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[illegible]

RESULT	11
LOCUS	H43753 478 bp mRNA EST
DEFINITION	VHJ691 rat Homeobox gene clone 188112, similar to pB12.4556
ACCESSION	IG HEAVY CHAIN V-11 REGION (HUMAN);
NID	H43753
KEYWORDS	q919d05
SOURCE	EST.
	human clone 188112 library-Sources broad INHIST vector-pT7+D

(Pharmacia) with a modified polylinker host-DH10H (ampicillin-resistant) primer-M3RRI RsrII-Not I RsrII-Eco RI Adult human 1st strand cDNA was primed with a Not I-Gligo(dT) primer [5].
5'-GAGTAATGGTGAACCTGAGCGCCCTTTTTTTTTTTT-3'
double stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of modified p773 vector (pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Patima Ronaldo.

ORGANISM

Eukaryotes
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonadata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominiinae; Homo.
1 (bases 1 to 478)

REFERENCE
Hillier, L., Clark, N., Duboucq, T., Ellington, K., Hawkins, M.,
Rogstad, M., Rastbach, M., Kennedy, T., LeMay, J., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Pohlring, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R.; Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stores: 379

Source: IMAGE Consortium, LLNL
This clone is available royalty-free

Location/Qualifiers
1..478

/organism="Homo sapiens"
/clone="18all2"

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h Similarity

179; Conservative 0; Mismatches 106; Indels 5; Gaps 33

GTGCGAGCTGCTCGAATCTGGTCTGAAGT - GAAGAAGCTTCGGTCTTGCGTTAAAGGTC 60

ctgctctgtctctgtgggtccatcaataatctactctgggaattggatccggcagtc 143

CTGCAGGGCCTCTGGAGGCAGCTTCAG-AGCTACAATTTCATTGGTGCGACAGGC 119

cagggaaagggaactggagtggtatgc-tat-tacagtgggaac-gccaacta 200

[illegible]

CACAGCAGGCTTTCAGGGCAATCATCAAAATTCTGTGTAATGACAGAAGCTA 239
- - - - -
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tgaagt tgaattctcttggaacacacggcgtctattactg 310

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Accession	Length	Species	EST	Date
I27727	290 bp	mpna		06-SEP-1995
EST13874		Homo sapiens	cdna 5'	end similar to immunoglobulin mu

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(gamma) heavy chain, v(IV)DJC regions (H1:305):
T27727
q609825
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EST.
human primer-M13 Reverse library=Human Testis.

Homo sapiens
Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Osteichthyes

Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo

1 (bases 1 to 209)
Adams, M. D., Kerlavage, A. P., Fleischmann, R. N., Fuldner, R. A.

Bult, C. J., Lee, N., Kirkness, E. F., Weinstock, K. G., Gokeyne, T. D., White, O., Sutton, G., Blake, J. A., Brandon, R. C., Chin, M.-W., Clayton, R. A., Cline, R. T., Cotton, M. D., Farley-Hughes, L., Fine, L.

Clayton, G. M., FitzGerald, L. M., FitzHugh, W. M., Fritchman, J. I., Geoghagen, N. S. M., Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E., Hinkle, Jr., P. S.,

Kelley, J. M., Klimek, K. M., Kelley, J. C., Liu, L.-I., Marmaros, S. M., Merrick, J. M., Moreno-Palancas, R. F., McDonald, L. A., Nguyen, D. T.,

Bellegirino, S. M., Phillips, C. A., Pyger, S. F., Scott, J. L.,
Saudek, D. M., Shirley, P., Small, K. V., Spriggs, T. A., Uiterback, T. H.

```

Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 139
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
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        1..169
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Matches 57; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
Db 100 aggtgccttgatcactctggagctgagatgaggaagcctggagct-cagtgaagctct 158
QY 2 AGGTGCAGCTGCTGAGCTGCTGCTGAGTGAAGAGCCCTGGCTCTGGCTGAAGTCT 61
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 159 cctgaccaggc 168
QY 62 CCTCAGGGC 71
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RESULT 14
LOCUS      R83139      303 bp      mRNA      EST      04-AUG-1995
DEFINITION YP11403 r1 Homo sapiens cDNA clone 187156 5' similar to gb-M52726
            IG HEAVY CHAIN V-III REGION (HUMAN);
ACCESSION  R83139
NID         928016
KEYWORDS    EST.
SOURCE      human clone-187156 library=Soares breast 3NBHST vector-pT73D
            (Pharmacia) with a modified polylinker host-DH10B (ampicillin
            resistant) primer-M13p1 Psite1-Not I Psite2-Eco RI Adult human
            1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
            TGTTACCATCTGAGTGGAGCGCGCCCTTTTITTTTTTTT 3'],
            double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
            digested with Not I and cloned into the Not I and Eco RI sites of a
            modified pT73 vector (Pharmacia). Library went through one round
            of normalization to a Cot = 20 Library constructed by Bento Soares
            and M.Fatima Bonaldo.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.
REFERENCE   1 (bases 1 to 303)
AUTHORS     Hillier,L., Clark,N., Dubouque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevisakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
            Wilson,R.
            The WashU-Merck EST Project
            Unpublished (1995)
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 111
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
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        1..303
        /organism="Homo sapiens"
        /clone="187156"
BASE COUNT      31 a   49 c   52 g   36 t   1 others
ORIGIN
Query Match      9.3%; Score 35; DB 69; Length 422;
Best Local Similarity 63.8%; Pred. No. 4.46e-25;
Matches 81; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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BASE COUNT      52 a   55 c   91 g   76 t   9 others
ORIGIN
Query Match      10.3%; Score 39; DB 51; Length 403;
Best Local Similarity 62.2%; Pred. No. 7.40e-32;
Matches 88; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
Db 112 aggtgccttgatcactctggagctgagatgaggaagcctggagct-cagtgaagctct 171
QY 2 AGGTGCAGCTGCTGAGCTGCTGAGTGAAGAGCCCTGGCTCTGGCTGAAGTCT 61
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 172 cctgaccaggcctggagctgagatgaggaagcctggagct-cagtgaagctgaagctgaagc 231
QY 62 CTGTCAGGCTGCTGAGCTGCTGAGTGAAGAGCTGAATATTAATTAATTAATTAATTAATTAAT 121
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 232 cctgaccaggcctggagctgagatgaggaagcctggagct-cagtgaagctgaagctgaagc 254
QY 122 CTGCACAGGCTCTTCACTGGATG 144
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
RESULT 15
LOCUS      H43952      422 bp      mRNA      EST      31-JUL-1995
DEFINITION Y07095 r1 Homo sapiens cDNA clone 184420 5' similar to gb-S55735
            IG ALPHA-1 CHAIN C REGION (HUMAN);
ACCESSION  H43952
NID         920004
KEYWORDS    EST.
SOURCE      human clone-183320 library=Soares breast 3NBHST vector-pT73D
            (Pharmacia) with a modified polylinker host-DH10B (ampicillin
            resistant) primer-M13p1 Psite1-Not I Psite2-Eco RI Adult human
            1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
            TGTTACCATCTGAGTGGAGCGCGCCCTTTTITTTTTTTT 3'],
            double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
            digested with Not I and cloned into the Not I and Eco RI sites of a
            modified pT73 vector (Pharmacia). Library went through one round
            of normalization to a Cot = 20 Library constructed by Bento Soares
            and M.Fatima Bonaldo.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.
REFERENCE   1 (bases 1 to 422)
AUTHORS     Hillier,L., Clark,N., Dubouque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevisakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
            Wilson,R.
            The WashU-Merck EST Project
            Unpublished (1995)
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 299
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
    source
        1..422
        /organism="Homo sapiens"
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BASE COUNT      87 a   135 c   115 g   82 t   3 others
ORIGIN
Query Match      9.3%; Score 35; DB 69; Length 422;
Best Local Similarity 63.8%; Pred. No. 4.46e-25;
Matches 81; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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US-08-844-215-27.rsta

Search completed: Tue Feb 24 13:29:00 1998
Job time : 587 secs.

MIPSREH

Release 2.1D John F. Collins, Biocomputing Research Unit
Copyright (C) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.
MIPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on Tue Feb 24 07:03:16 1998. MaxPar time 6.87 seconds
266 870 Million cell updates/sec
Tubular output not generated.
Title: >US-08-844-215-1
Description: (1-132) from US0884215.pcp
Perfect Score: 956
Sequence: 1 EVOLLEQSGAEVKEPKGVSK.....RCYPGFQWGGTIVTVSS 132

Scoring table: PAM 150
Gap 11
Searched: 111726 seqs, 13989129 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
Statistics: Mean 30.964; Variance 153.640; scale 0.202
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query		DB	ID	Description	Pred. No.
		Match	Length				
1	696	72.8	481	5	R24442	Sequence of antibody	1.37e-47
2	559	58.5	120	9	R54795	SpA-reactive IgM heavy	4.30e-36
3	557	58.3	476	6	R31023	Antibody D heavy chain	6.32e-36
4	549	57.4	123	23	W19889	CEA-specific antibody	2.94e-35
5	537	56.2	98	12	R75068	Dp10 VH region.	2.94e-34
6	534	55.9	123	23	W19881	CEA-specific antibody	5.22e-34
7	533	55.8	123	23	W19889	CEA-specific antibody	6.34e-34
8	532	55.6	123	23	W19887	CEA-specific antibody	7.63e-34
9	530	55.4	124	23	W19886	CEA-specific antibody	1.13e-33
10	529	55.3	147	12	R65019	93KA9 anti-Varicella	1.37e-33
11	526	55.0	110	23	W13536	Anti-melanoma antibody	2.43e-33
12	521	54.5	124	9	R45610	Monoclonal antibody G	6.32e-33
13	515	53.9	98	12	R75069	HV126? VH region.	2.00e-32
14	515	53.9	117	4	R23358	Protein encoded by th	2.00e-32
15	515	53.9	117	4	R28623	Human heavy chain V	2.00e-32
16	515	53.9	117	20	W03950	DNA fragment vH49 8,	2.00e-32
17	515	53.9	122	0	R75964	HSV-neutralising anti	2.00e-32
18	513	53.7	120	9	P54745	SpA-reactive IgM heavy	2.94e-32
19	512	53.6	121	14	P7-874	Humanised mouse IgG2	3.54e-32
20	512	53.6	140	9	P55555	DPEN-200 Humanised an	3.54e-32

21	511	53.5	145	22	W23841	Human anti-tumour ant	4.25e-32
22	506	52.9	143	23	W21847	Humanised heavy chain	1.11e-31
23	505	52.9	142	9	P50189	Heavy chain variable	1.75e-31
24	503	52.6	249	14	P77610	Humanised 5G1.1 VH +	1.98e-31
25	494	51.7	142	9	P50194	Heavy chain variable	1.11e-30
26	493	51.6	249	14	P77615	Humanised 5G1.1 VH +	1.75e-30
27	489	51.2	142	9	P50194	Heavy chain variable	1.11e-30
28	489	51.2	142	9	P50194	Heavy chain variable	1.11e-30
29	489	51.2	142	9	P50194	Heavy chain variable	1.11e-30
30	489	51.2	142	9	P50194	Heavy chain variable	1.11e-30
31	489	51.2	142	9	P50194	Heavy chain variable	1.11e-30
32	488	51.0	140	23	W21849	Humanised heavy chain	2.88e-30
33	488	51.0	242	7	P32567	Humanised 5G1.1 VH +	2.88e-30
34	488	51.0	242	7	P32567	Humanised 5G1.1 VH +	2.88e-30
35	488	51.0	242	7	P32567	Humanised 5G1.1 VH +	2.88e-30
36	487	50.9	142	9	P50194	Heavy chain variable	1.11e-30
37	487	50.9	142	9	P50194	Heavy chain variable	1.11e-30
38	483	50.5	142	9	P50194	Heavy chain variable	1.11e-30
39	482	50.4	142	9	P50194	Heavy chain variable	1.11e-30
40	481	50.3	142	9	P50194	Heavy chain variable	1.11e-30
41	479	50.1	139	8	P43693	pH1.3/Humanised heavy	1.64e-29
42	479	50.1	139	8	P43693	pH1.3/Humanised heavy	1.64e-29
43	478	50.0	139	11	R62678	Humanised heavy chain	2.35e-29
44	478	50.0	139	11	R62678	Humanised heavy chain	2.35e-29
45	478	50.0	279	19	W05826	Humanised W291 antiBo	2.35e-29

ALIGNMENTS

RESULT 1
ID R24442 standard; Protein: 481 AA.
AC R24442;
DT 02-JAN-1992 (first entry)
DE Sequence of antibody molecule IgG1.
KW Antibody; immunoglobulin G1.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 308
FT /label= N
FT /note= "Substn. to create glycan addition site"
FT Misc-difference 310
FT /label= S
FT /note= "see above"
FT Misc-difference 321
FT /label= N
FT /note= "see above"
FT Misc-difference 329
FT /label= N
FT /note= "see above"
FT Misc-difference 331
FT /label= S
FT /note= "see above"
FT Misc-difference 356
FT /label= N
FT /note= "see above"
FT Misc-difference 369
FT /label= N
FT /note= "see above"
FT Misc-difference 393
FT /label= N
FT /note= "see above"
FT Misc-difference 393-A.
PD 11-JUN-1992.
PF 18-NOV-1991. 308605.
PR 22-NOV-1990; US-618314.
PA (GENE) GEN HOSPITAL CORP.
PI Seed B, Walz G.
PI WFI 92-016789/26.
DR WFSB; Q25443.
DR Inhibition of cell adhesion mediated through EAM-1 mol. binding
PI - used in treating chronic inflammation, rheumatoid arthritis,
PT psoriasis, etc.
PS Disclousure, Fig 1, 46pp, English.
CC The IgG1 in its nascent form, bears no staphylococcal chains. The
CC Inverters designed a molecule including several such sites for
CC attachment of staphylococcal chains (see R24442, FT). The

[illegible]

Query Match	58.3%	Score 557	DB 6	Length 476
Best Local Similarity	64.4%	Pred. No. 6,32e-36		
Matches	85	Conservative	19	Mismatches 23
			Indels	5
			Gaps	3
Db	20	qmqqv-qsgaevkbpqssvsvtsckasqgftfnysaivswrqaaqalwmgqilpittqpt	78	
Qy	1	EVQLLESGAEVRFKFGSSVAVSPKASQTEFGHVTWVDPAPQGLHWGESLPFGSAN	60	
Db	79	ysqnf-q---grvltadkatsstahmeltsrsedtaavyycatdryrqaufdravqwid	114	
Qy	61	YAQNYAOKFRDVRSLIADBESTSTFELSRLSDDTAVYICADDPHYCSAGKCYGPFQ	120	
Db	135	pwagatlvtyss	146	


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QY 121 QWGGQTLVTVSS 132
|||||
RESULT 4
ID W19888 standard; Protein; 123 AA.
AC W19888:
DE 07-DEC-1997 (first entry)
DE CEA-specific antibody CEA6 VH mutant HBB11 sequence.
KW Carcinoembryonic antigen; CEA; human; antibody; scFv;
KW tumour marker; lung cancer; breast cancer; colon cancer;
KW adenocarcinoma; diagnosis.
KW Chimeric Homo sapiens;
OS Chimeric synthetic.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT Region 50..66
FT /label= CDR2
FT /label= CDR3
PN W09720932-A1.
PD 12-JUN-1997.
PR 09-DEC-1996; G03043.
PR 11-OCT-1996; GR-021295.
PR 07-DEC-1995; GR-025004.
PR 23-MAY-1996; GR-010824.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Allen DJ, McCafferty JG, Osbourn JK.
DR WPI: 97-319779/29.
PT Specific binding members for human carcinoembryonic antigen - bind
PT to the A3-B3 extracellular domain of hCEA and are substantially
PT non-cross-reactive with human liver cells; used for diagnosing
PT cancer.
PS Claim 4; Fig 2; 128pp; English.
CC This polypeptide sequence comprises the heavy chain variable region
CC (VH), HBB11, obtained by mutagenesis of the VH CDR3 of human
CC carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see
CC W19888). A claimed specific binding member (A) comprises an hCEA
CC specific antibody antigen binding domain that has a dissociation
CC constant for hCEA of less than 1 x 10-8 M, is non-cross-reactive
CC with human liver cells, and preferentially binds to the A3-B3
CC extracellular domain of hCEA and/or to cell-associated hCEA over
CC hCEA over soluble hCEA. Preferred (A) include pairings of VH and
CC VL sequences from CEA1-7 (see W19875-85), or their CDR sequences,
CC as well as CEA6 VH and VL variants (see W19886-95) obtained by
CC mutagenesis or chain shuffling. An example of a claimed pairing
CC is HBB11 VH with CEA6 VL. (A) is used to detect cells expressing
CC hCEA, in vivo or in vitro, especially tumour cells for diagnosing
CC cancer, e.g. adenocarcinoma of the colon, lung or breast.
SQ Sequence 123 AA;

Query Match 57.4%, Score 549, DB 23, Length 123,
Best Local Similarity 56.7%, Pred No. 2,94e-35;
Matches 86; Conservative 16; Mismatches 19; Indels 9; Gaps 5;

Db 1 qvqlv-qsgaevkpgssvkscasgtfssvaylswwrqpggglewmgsilpifgtan 59
:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLEQSGAEVRPKPSSSVKVSCTKAS33IFSGHVITWVPLAPG3LEWMGDSIFP3SAN 60
60 yaq----kfgrvltitadeststymelsrdsctavvyvcar 98
||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YAQNYAQKFPDPVSTIADSTSTSFILSNLPSDTAVVYCAP 103

RESULT 6
ID W19881 standard; Protein; 123 AA.
AC W19881:
DE 07-DEC-1997 (first entry)
DE CEA-specific antibody CEA6 VH sequence.
KW Carcinoembryonic antigen; CEA; human; antibody; scFv;
KW tumour marker; lung cancer; breast cancer; colon cancer;
KW adenocarcinoma; diagnosis.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 50..66
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT /note= "complementarity determining region 3"
FT /label= CDR3
FT /note= "complementarity determining region 3"
PN W09720932-A1.
PD 12-JUN-1997.
PR 09-DEC-1996; G03043.
PR 11-OCT-1996; GR-021295.
PR 07-DEC-1995; GR-025004.
PR 23-MAY-1996; GR-010824.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Allen DJ, McCafferty JG, Osbourn JK;

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Query Match 55.8%; Score 533; DB 23; Length 12;
Best Local Similarity 65.9%; Pred. No. 6,34e-34;
Matches 87; Conservative 17; Mismatches 19; Indels 9; Gaps 5;

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1 qvqiv-qsgaevkpyssvkcskaqgtfnsnpinwlrqapqqlwmuusiipstqtun 50
Db
1 EVQLLEGGSGAEVFKPSSVKVSKAKSGITFSGRVITWVQAPGQGIPLWVGESIPFGAS 60
QY
60 yaq---kfgrtitadeststamelsirsdetavycagshly el-yyy-ymd 111
Db
61 YAGNVACKFEPKRVYSITACDSTSPFESNIPSMITAVVYCARPPKPVYCAKGRIFPG 120
QY

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RESULT	8	
W19887	standard; Protein: 123 AA.	
W19887		
07-DEC-1997	(first entry)	
DE	CEA-specific antibody CEA6 VH mutant HBAll sequence.	
DE	Carcinoembryonic antigen; CEA; human; antibody; scFv;	
KK	tumour marker; lung cancer; breast cancer; colon cancer;	
KK	adenocarcinoma; diagnosis.	
OS	Chimeric Homo sapiens:	
OS	Chimeric synthetic	
Key	Location/Qualifiers	
FFH	Region	31...35
FT	/label= CDR1	
FT	/note= "complementarity determining region 1"	
FT	Region	50...66
FT	/label= CDR2	
FT	/note= "complementarity determining region 2"	
FT	Region	99...112
FT	/label= CDR3	
FT	/note= "complementarity determining region 3"	
FT	W09720932-A1.	
PD	12-JUN-1997.	
PP	09-DEC-1996; G03043.	
PP	11-OCT-1996; GR-021205.	
PP	07-DEC-1995; GB-025004.	
PR	23-MAY-1996; GB-010824.	
PPA	(CAMP-) CAMPEDIGE ANTIBODY TECHNOLOGY.	
PPA	Allen BJ, McGafferty JC, Osburn W;	
DR	WPI; 97-319779/29.	
FT	Specific binding members for human carcinoembryonic antigen - bind	
FT	to the A3-B3 extracellular domain of hCEA and are substantially	
PT	non-cross-reactive with human liver cells; used for diagnosing	
PT	Cancer	
PI	claim 4; Fig 2: 128pp; English.	
CCC	This polypeptide sequence comprises the heavy chain variable region	
CCC	(VH), obtained by mutagenesis of the VH (CDR3) of human	

CC carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see
 CC W19881). A claimed specific binding member (A) comprises an hCEA
 CC specific antibody antigen binding domain that has a dissociation
 CC constant for hCEA of less than 1×10^{-8} M, is non-cross-reactive
 CC with human liver cells, and preferentially binds to the A3-B3
 CC extracellular domain of hCEA and/or to cell-associated hCEA over
 CC hCEA over soluble hCEA. Preferred (A) include pairings of VH and
 CC VL sequences from CEA1-7 (see W19876-85), or their CDR sequences,
 CC as well as CEA6 VH and VL variants (see W19886-95) obtained by
 CC mutagenesis or chain shuffling. (A) is used to detect cells
 CC expressing hCEA, in vivo or in vitro, especially tumour cells for
 CC diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast.
 CC Sequence 123 AA;

Query Match 55.5%; Score 530; DB 23; Length 123;
 Best Local Similarity 65.9%; Pred. No. 7 58e-14;
 Matches 87; Conservative 19; Mismatches 17; Indels 9; Gaps 5;

Db 1 qvqlv-qsgaevkbpssvkvscasggtfnsfnlwrqapggglewmgslpsfgtan 59
 QY 1 EVOLLOSAGAEVKRPSSVSKASGGTFSGHVITWVPQAPGQGLEWVGSIPIFGSAN 60

Db 60 yaq----kfgrlritadeststymelssrsedtavyyca-gans-cn--rsyyyymd 111
 QY 61 YAGNYAKKFPORVSIADSTSTSFIELSNLPSDITAVYYCARPPKYSAGKCYPGFPQ 120

Db 112 vraggtmtvss 123
 QY 121 QWGGGILTVSS 132

RESULT 9
 ID W19896 standard; Protein: 123 AA.
 AC W19886;
 DE CEA-specific antibody CEA6 VH mutant T6D10 sequence.
 KW Carcinoembryonic antigen; CEA; human; antibody; serf;
 KW tumour marker; lung cancer; breast cancer; colon cancer;
 KW adenocarcinoma; diagnosis.
 OS Chimeric Homo sapiens;
 OS Chimeric synthetic.
 FH Key Location/Qualifiers
 FT Region 31..45
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 50..66
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 69..112
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 PN W0920932-A1
 PD 12-JUN-1997
 PF 09-DEC-1996; G03043
 PR 11-OCT-1994; GB-021295.
 PR 07-DEC-1995; GB-025004.
 PR 23-MAY-1996; GB-010824.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Allen DJ, McCafferty JG, Osbourn JK.
 DP WPI: 97-010799/29
 PT Specific binding members for human carcinoembryonic antigen - bind
 PT to the A3-B3 extracellular domain of hCEA and are substantially
 PT non-cross-reactive with human liver cells; used for diagnosing
 PT cancer
 PS Claim 4; Fig 2; 128pp; English.
 CC This polypeptide sequence comprises the heavy chain variable region
 CC (VH), T6D10, obtained by mutagenesis of the VH CDR3 of human
 CC carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see
 CC W19881). A claimed specific binding member (A) comprises an hCEA
 CC specific antibody antigen binding domain that has a dissociation
 CC constant for hCEA of less than 1×10^{-8} M, is non-cross-reactive
 CC with human liver cells, and preferentially binds to the A3-B3
 CC extracellular domain of hCEA and/or to cell-associated hCEA over

CC hCEA over soluble hCEA. Preferred (A) include pairings of VH and
 CC VL sequences from CEA1-7 (see W19876-85), or their CDR sequences,
 CC as well as CEA6 VH and VL variants (see W19886-95) obtained by
 CC mutagenesis or chain shuffling. Examples of claimed pairings are
 CC T6D10 VH with T6D12 or CEA6 VL. (A) is used to detect cells
 CC expressing hCEA, in vivo or in vitro, especially tumour cells for
 CC diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast.
 CC Sequence 123 AA;

Query Match 55.4%; Score 530; DB 23; Length 123;
 Best Local Similarity 65.9%; Pred. No. 1.13e-33;
 Matches 87; Conservative 17; Mismatches 19; Indels 9; Gaps 5;

Db 1 qvqlv-qsgaevkbpssvkvscasggtfnsfnlwrqapggglewmgslpsfgtan 59
 QY 1 EVOLLOSAGAEVKRPSSVSKASGGTFSGHVITWVPQAPGQGLEWVGSIPIFGSAN 60

Db 60 yaq----kfgrlritadeststymelssrsedtavyyca-gans-cn--rsyyyymd 111
 QY 61 YAGNYAKKFPORVSIADSTSTSFIELSNLPSDITAVYYCARPPKYSAGKCYPGFPQ 120

Db 112 vraggtmtvss 123
 QY 121 QWGGGILTVSS 132

RESULT 10
 ID R65019 standard; Protein: 147 AA.
 AC R65019;
 DT 02-OCT-1995 (first entry)
 DE 93KA9 anti-Varicella zoster virus antibody heavy chain variable.
 DE region.
 KW Varicella zoster virus; VZV; anti-VZV monoclonal antibody; 93KA9;
 KW glycoprotein II subunit; vaccine.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Protein 20..147
 FT /label= mature light chain
 FT Region 50..54
 FT /label= complementarity determining region (CDR)
 FT Region 69..85
 FT /label= CDR
 FT Region 118..136
 FT /label= CDR
 FT /label= CDR
 PN W09504080-A.
 PD 09-FEB-1995.
 PF 22-JUL-1994; U08241.
 PR 28-JUL-1993; US-098479.
 PR 24-MAY-1994; US-217918.
 PA (SANO) SANDOZ PHARM CORP.
 PI Lake P, Ostberg L;
 DP WPI: 95-090612/12.
 DR N-PSDB; Q82750.
 PT Human monoclonal antibodies specific for the glycoprotein II
 PT subunit of varicella zoster virus - used in a therapy and
 PT prophylaxis of infection
 PS Claim 8; Fig 4B; 39pp; English.
 CC A human anti-Varicella zoster virus monoclonal antibody was prepd.
 CC using the trioma method of Ostberg et al. (1983) Hybridoma 2:361-367.
 CC One resultant trioma neutralised VZV in the absence of complement.
 CC This cell line, designated cell line IC93KA9, produced an antibody
 CC designated 93KA9. cDNA for the light and heavy chain variable region
 CC genes of the 93KA9 antibody were cloned using PCR. At least two
 CC heavy chain (gamma-1) and two light chain (kappa) specific clones
 CC were sequenced (see Q82749 & Q82750 respectively).
 CC Sequence 147 AA;

Query Match 55.3%; Score 529; DB 12; Length 147;
 Best Local Similarity 64.2%; Pred. No. 1.37e-33;
 Matches 86; Conservative 20; Mismatches 20; Indels 9; Gaps 6;

Db 20 qvqlv-qsgaevkbpssvkvscasggtfnsfnlwrqapggglewmgslpsfgtan 77
 QY 21 EVOLLOSAGAEVKRPSSVSKASGGTFSGHVITWVPQAPGQGLEWVGSIPIFGSAN 80

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QY 1 EVOLLEQSGAEVKKPSSVKVSCKASGGSFTSGSHVITWVRQAPGQGLGWGMSIPIFGSAN 60
Db 78 -t--yqkfggrvtisadastaymelslrdsddtdamyyccardita-pgaaptplniyg 133
QY 61 YAUHYAKKFPKPVSIIADESTISFIELNLSRGTAVVYCAKAPKPKYASAGRYVQFF- 119
Db 134 mdvwgggtttvss 147
QY 120 QQ-WGQGLTVTVSS 132

RESULT 11
ID W13536 standard; protein: 119 AA.
AC W13536;
DT 28-OCT-1997 (first entry)
DE Anti-melanoma antibody 2-71 from VH antibody fusion phage library.
KW Human; monoclonal antitumor antibody; peripheral blood lymphocyte.
KW cancer; tumorigenesis; anticancer vaccine.
OS Homo sapiens.
PN WO9702479-A2.
PD 23-JAN-1997
PF 28-JUN-1996; IB1032.
PR 30-JUN-1995; US-497647.
PA (UYVA ) UNIV VALE.
PI Cai X, Garen A.
PI WPI: 97-109061/10.
DR
PT Prodn. of human monoclonal anti-tumor antibodies - by screening a
PT fusion phage library produced using peripheral blood lymphocytes
PT from a cancer patient
PS Claim 19; Page 75:76; 82pp; English.
CC A process for isolating and synthesizing human monoclonal anti-tumor
CC antibodies has been produced. The process involves: (a) constructing at
CC least one fusion phage library from the peripheral blood lymphocytes
CC (PBUs) of a cancer patient; (b) screening for anti-tumor antibodies in
CC the phage library in a binding assay with cultured tumor cells of the
CC same type as the patient's tumor; (c) removing extraneous antibodies by
CC absorption against normal human cells; (d) cloning the phage selected in
CC step (b) and (c); (e) assaying the specificity of the cloned phage by
CC incubating the phage with at least two types of cultured normal cells;
CC and (f) further testing the specificity of cloned phage that do not bind
CC to either cell line of cultured normal cells in further binding assays
CC to cultured tumor cells derived from more than one other tumor that is
CC not the patient's tumor. The present sequence represents a human heavy
CC chain antibody, from a VH antibody fusion phage library, produced by
CC a method as described above. The antibodies produced can be used for
CC diagnostic and therapeutic applications and for isolating tumor
CC antigens for studying tumorigenesis or for use as anti-cancer vaccines.
CC The human antibodies have low immunogenicity in humans compared to
CC murine monoclonal antibodies (MABs). Since the antibodies are isolated
CC from fusion phage libraries, their affinity and specificity for a
CC tumor cell line can be improved by genetic manipulations.
SQ Sequence 119 AA;

Query Match 55.0%; Score 526; DB 23; Length 119.
Best Local Similarity 69.6%; Pred No 2 43e-33;
Matches 87; Conservative 16; Mismatches 10; Indels 12; Gaps 4;

Db 7 gglevkkpssvkvscasggftssyaiswvqagqglwmggllpifqtanvaq---- 62
QY 8 SGAEVKPSSVKVSKASGGIFSGSHVITWVRQAPGQGLGWGMSIPIFGSANYAQNVAQ 67
Db 63 kfggrvtitadkststamelslrdsdttavvycaar-----qgar-ydaf-diwgqatl 114
QY 68 KFPDRVSIIADESTISFIELNLSRGTAVVYCAKAPKPKYASAGRYVQFFQWGGTIL 127
Db 115 vtvs 119
QY 128 VTVSS 132

RESULT 12
ID R45610 standard; protein: 124 AA.
AC R45610;

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DT 22-JUL-1994 (first entry)
DE Monoclonal antibody GP68 heavy chain (V H 1).
KW HIV; Human Immunodeficiency Virus; gp120; glycoprotein;
KW envelope protein; monoclonal antibody; MAb; vaccine; therapy.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR 1
FT Region 50..66
FT /label= CDR 2.
FT Region 99..110
FT /label= CDR 3.
FT Region 111..124
FT /label= Framework IV, JH4 segment.
PN EP-581353-A.
PD 02-FEB-1994.
PF 05-JUL-1993; 201959.
PR 03-JUL-1992; EP-202032.
PA (NEWE-) NEDERLANDEN, MIN WELZIJN.
PI Osterhaus ADME;
PI WPI: 94-036603/05.
DB N-PSDB; Q55663.
CC Monoclonal antibodies to HIV-1 - directed against glyco:protein
CC gp120, useful for passive immunotherapy or prodn. of
CC anti-idiotype vaccines
CC Claim 6; Page 22-23; 34pp; English.
CC The monoclonal antibodies (MAB's) designated GP13, GP44 and GP68
CC react with HIV-1 gp120 glycoprotein variants containing the amino
CC acids Asn88, Lys117, Asn262 and Tyr 435 but exhibit at least 50%
CC reduced reaction with gp120 variants in which these amino acids
CC have been deleted or substituted. The MAB's are useful for passive
CC immunotherapy and their anti-idiotype antibodies can be used in the
CC production of vaccines.
SQ Sequence 124 AA;

Query Match 54.5%; Score 521; DB 9; Length 124.
Best Local Similarity 62.9%; Pred. No. 6 32e-33;
Matches 83; Conservative 19; Mismatches 22; Indels 8; Gaps 6;

Db 1 qvqlv-qsgaevkpkssvkvscasggftssstlhwvrtqpgqglwmmkiiptlssst 59
QY 1 EVOLLEQSGAEVKKPSSVKVSCKASGGSFTSGSHVITWVRQAPGQGLGWGMSIPIFGSAN 60
Db 60 yspqf-q---grvltladeststvmelsqtsadtavvyckasqaswslirs-pc-id 112
QY 61 YAUHYAKKFPKPVSIIADESTISFIELNLSRGTAVVYCAKAPKPKYASAGRYVQFFQ 127
Db 113 nwdgggtltvss 124
QY 121 QWGGTILTVSS 132

RESULT 13
ID P72069 standard; protein: 98 AA.
AC P72069;
DT 26-SEP-1995 (first entry)
DE HV1263 VH region.
KW Graves ophthalmopathy associated immunoglobulin protein;
KW orbital antigen; monoclonal antibody; heavy chain; H chain;
KW variable region; autoimmunity.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT Region 50..66
FT /label= CDR2
PN WO9508336-A.
PD 30-MAR-1995.
PF 22-SEP-1994; U10756.
PR 22-SEP-1993; US-124469.
PA (NICH-) NICHOLS INST DIAGNOSTICS.
PI Melachlan SM, Rapoport B;
PI WPI: 95-139383/18.

```

DR N-PSDB; Q89328.
 PT Graves' ophthalmopathy-associated monoclonal antibody - produced
 PT by molecular cloning of immunoglobulin genes by PCR
 PS Disclosure: Page 69; 94pp; English.
 CC L- and H-chain DNA was amplified by PCR from Graves' orbital
 CC tissue and clones encoding autoimmune-associated immunoglobulin
 CC fragments were obtained. 13/15 clones of H chain (IgG1) genes
 CC showed homology to the closest germline genes, DP10 (Q89327) and
 CC hV1262 (Q89328). The DNA (Q89329) and corresp. amino acid
 CC (R72070) sequences of the VH region of a representative clone,
 CC QF7H1.2, are provided.
 SQ Sequence 98 AA;

Query Match 53.9%; Score 515; DB 12; Length 98;
 Best Local Similarity 74.8%; Pred. No. 2,00e-32;
 Matches 77; Conservative 13; Mismatches 8; Indels 5; Gaps 4;

Db 1 qvqlv-qsgaevkpkqssvkvsckasggtfssyaisvwrqapggqlewmgrilpg-i- 57
 QY 1 EVULLEQSGAEVFKPKPSSVKVSKASGGTFSSGHVITWVPQAPQVLEWMSPIPIFGSAN 60

Db 58 -a-nyackfggrvtitadkstststymelsslrscdtavyyccar 98
 QY 61 YACNYACKFPDPVSYIIADESTSTSFTELSNLPSSDTAVYYCAP 103

RESULT 14
 ID R22358 standard; Protein: 117 AA.

AC R22358;
 DT 17-AUG-1992 (first entry)
 DE Protein encoded by the human heavy chain V region gene VH49.8.
 KW Heavy chain: variable region; VH1 family.
 OS Homo sapiens.
 PN WC9203918-A.
 PD 19-MAR-1992.
 PE 28-AUG-1991; U06185.
 PF 29-AUG-1990; YS-574748.
 PR 31-AUG-1990; HS-575062
 PA (GENP-) GENPHARM INT INC
 PI Lonberg N. Kay R;
 DR WPI: 92-113362/14.
 DP N-PSDB: Q22419
 PT Immunoglobulin transgenes - for prodn. of heterologous
 PT non-rearranged and/or rearranged Ig chains
 PS Example 14; Page 87; 172pp; English.
 CC The human placental genomic DNA library cloned into the phage
 CC vector lambda FIX II was screened with the human VH1 family
 CC specific oligonucleotide (see Q22418). Phage clone lambda
 CC 49.8 was isolated and a 6.1 kb XbaI fragment contg. the variable
 CC segment VH49.8 subcloned into pNN03 to generate plasmid pVH49.8.
 CC An 800 bp region of this insert was sequenced. VH49.8 was found
 CC to have an open reading frame which encoded the sequence shown..
 SQ Sequence 117 AA;

Query Match 53.9%; Score 515; DB 4; Length 117;
 Best Local Similarity 74.8%; Pred. No. 2,00e-32;
 Matches 77; Conservative 13; Mismatches 8; Indels 5; Gaps 4;

Db 20 qvqlv-qsgaevkpkqssvkvsckasggtfssyaisvwrqapggqlewmgrilpg-i- 76
 QY 1 EVULLEQSGAEVFKPKPSSVKVSKASGGTFSSGHVITWVPQAPQVLEWMSPIPIFGSAN 60

Db 77 -a-nyackfggrvtitadkstststymelsslrscdtavyyccar 117
 QY 61 YACNYACKFPDPVSYIIADESTSTSFTELSNLPSSDTAVYYCAP 103

RESULT 15
 ID R38623 standard; Protein: 117 AA.
 AC R38623;
 DT 10-NOV-1993 (first entry)
 DE Human heavy chain V region VH49.8.
 KW Immunoglobulin; IgG; heavy chain; minilocus transgene;

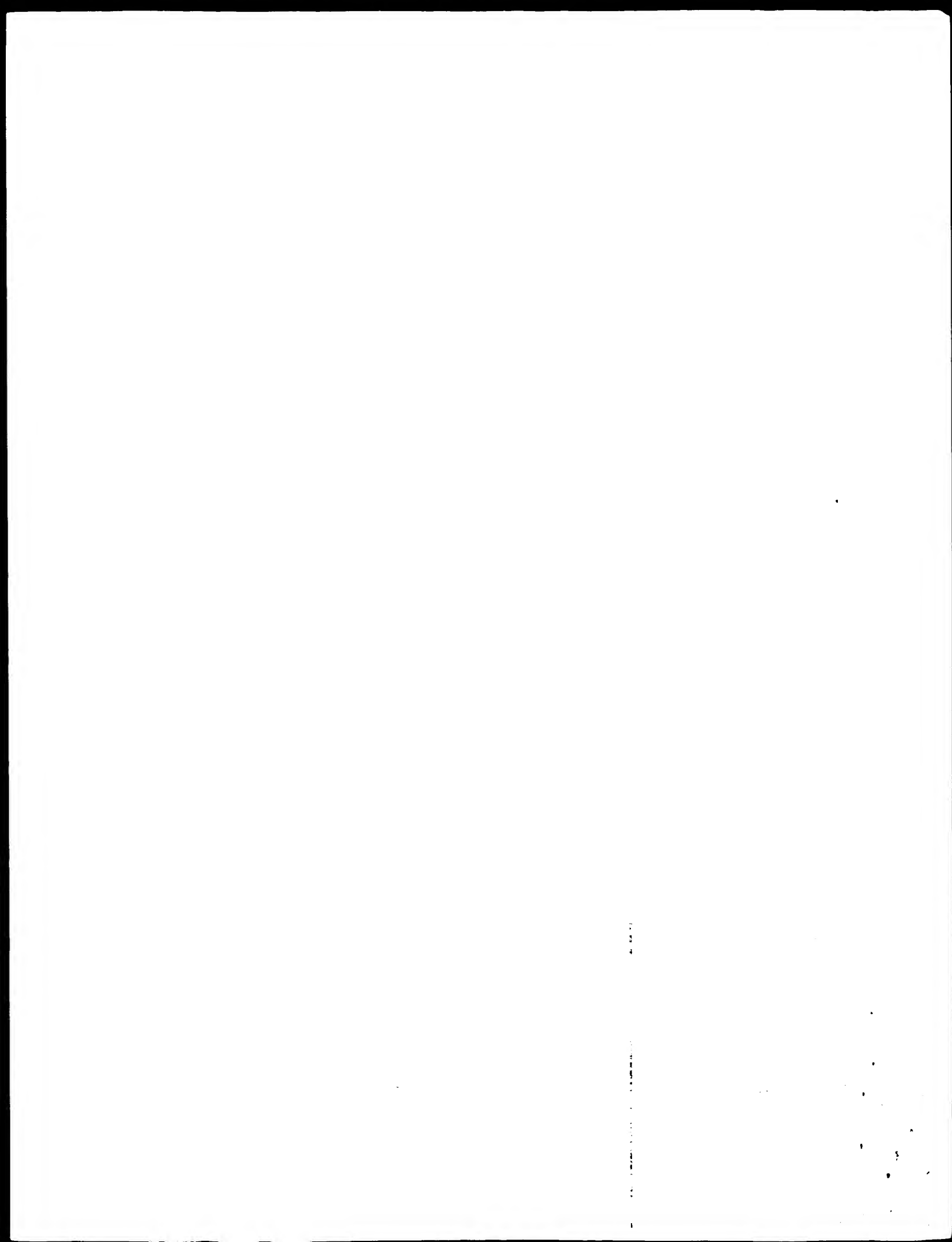
KW isotype switching; H chain variable region.
 OS Homo sapiens.
 PN WC9312227-A.
 PD 24-JUN-1993.
 PE 17-DEC-1992; U10983.
 PR 17-DEC-1991; US-810279.
 PR 18-MAR-1992; US-853408.
 PR 23-JUN-1992; US-904068.
 PA (GENP-) GENPHARM INT INC.
 PI Kay RM, Lonberg N;
 DR WPI: 93-214169/26.
 DP N-PSDB: Q44185.
 PT Transgenic non-human animals contg. immunoglobulin heavy chain
 PT transgene - used to produce useful antibodies by isotype
 PT switching
 FS Example 12, Page 96; 196pp; English.
 CC A human placental genomic DNA library cloned into the phage vector
 CC lambda FIX II was screened with the human VH1 family specific
 CC oligonucleotide Q44184. Phage clone lambda 49.8 was isolated and a
 CC 6.1 kb XbaI fragment containing the variable segment VH49.8 was
 CC subcloned into pNN03 to generate plasmid pVH49.8. An 800bp
 CC region of this insert was sequenced (Q44185) and VH49.8 found to
 CC have an open reading frame and intact splicing and recombination
 CC signals, indicating that the gene is functional. Amino acid
 CC sequence Q44185 was deduced from the coding sequence; the last 3
 CC codons before the termination codon have not been translated.
 SQ Sequence 117 AA;

Query Match 53.9%; Score 515; DB 7; Length 117;
 Best Local Similarity 74.8%; Pred. No. 2,00e-32;
 Matches 77; Conservative 13; Mismatches 8; Indels 5; Gaps 4;

Db 20 qvqlv-qsgaevkpkqssvkvsckasggtfssyaisvwrqapggqlewmgrilpg-i- 76
 QY 1 EVULLEQSGAEVFKPKPSSVKVSKASGGTFSSGHVITWVPQAPQVLEWMSPIPIFGSAN 60

Db 77 -a-nyackfggrvtitadkstststymelsslrscdtavyyccar 117
 QY 61 YACNYACKFPDPVSYIIADESTSTSFTELSNLPSSDTAVYYCAP 103

Search completed: Tue Feb 24 07:03:57 1998
 Job time : 41 secs.



[MORF] (1M)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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Distribution rights by IntelligentGenetics, Inc.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:31:49 1998: MasPar time 3.19 Seconds
210,908 Million cell updates/sec

Tabular output not generated.

Title: >US-08-844-215-1
Description: (1-132) from US08844215.pep
Perfect Score: 956
Sequence: 1 EVOLLEQSGAEVXKPGSSVK PCYPGFQNGQGLIVSS 132

Scoring table: PAM 150
Gap 11

Searched: 56402 seqs, 5095871 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:Back1 2.51 3.52 4.53 5.54 6.55 7.56 8.57 9.58 10.59
10 PCT92 11 PCT93 12 PCT94 13 PCT95 14 PCT96

Statistics: Mean 28.605 Variance 140.983 scale 0.203

Pred No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	607	63.5	129.13	PCT-US95-0	Sequence 45, Application	2.43e-41
2	559	58.5	120.11	PCT-US93-1	Sequence 13, Application	2.79e-37
3	539	56.4	120.11	PCT-US93-1	Sequence 12, Application	1.36e-35
4	529	55.3	147.6	US-08-477	Sequence 47, Application	9.44e-33
5	515	53.9	102.10	PCT-US92-0	Sequence 63, Application	1.42e-33
6	515	53.9	102.10	PCT-US92-0	Sequence 55, Application	1.42e-33
7	515	53.9	102.7	US-07-834	Sequence 63, Application	1.42e-33
8	515	53.9	102.7	US-08-053	Sequence 63, Application	1.42e-33
9	515	53.9	122.12	PCT-US95-0	Sequence 8, Application	2.54e-33
10	512	53.6	121.11	PCT-US93-1	Sequence 15, Application	2.54e-33
11	512	53.6	140.11	PCT-US93-1	Sequence 4, Application	2.54e-33
12	489	51.2	117.6	US-08-477	Sequence 15, Application	2.17e-31
13	489	51.2	117.6	US-08-477	Sequence 15, Application	2.17e-31
14	489	51.2	117.6	US-07-634	Sequence 15, Application	2.17e-31
15	489	51.2	117.6	US-07-634	Sequence 72, Application	2.17e-31
16	489	51.2	117.6	US-08-477	Sequence 104, Application	2.17e-31
17	489	51.2	117.6	US-07-634	Sequence 4, Application	2.17e-31
18	489	51.2	117.6	US-08-477	Sequence 4, Application	2.17e-31
19	489	51.2	117.6	US-08-477	Sequence 72, Application	2.17e-31
20	489	51.2	117.6	US-08-477	Sequence 104, Application	2.17e-31
21	489	51.2	117.6	US-08-477	Sequence 15, Application	2.17e-31
22	489	51.2	117.6	US-08-477	Sequence 4, Application	2.17e-31

23	489	51.2	117.6	US-08-487	Sequence 15, Application	2.17e-31
24	489	51.2	117.6	US-08-487	Sequence 72, Application	2.17e-31
25	489	51.2	117.6	US-08-487	Sequence 104, Application	2.17e-31
26	489	51.2	117.6	US-08-487	Sequence 72, Application	2.17e-31
27	489	51.2	117.6	US-07-634	Sequence 104, Application	2.17e-31
28	481	50.3	121.6	US-07-634	Sequence 53, Application	1.02e-30
29	481	50.3	121.6	US-08-487	Sequence 53, Application	1.02e-30
30	481	50.3	121.6	US-08-474	Sequence 53, Application	1.02e-30
31	481	50.3	121.6	US-08-477	Sequence 53, Application	1.02e-30
32	476	49.8	116.6	US-08-487	Sequence 5, Application	4.57e-30
33	476	49.8	116.6	US-07-634	Sequence 6, Application	2.67e-30
34	476	49.8	116.6	US-08-477	Sequence 6, Application	2.67e-30
35	476	49.8	116.6	US-08-474	Sequence 6, Application	2.67e-30
36	476	49.8	140.6	US-07-945	Sequence 28, Application	2.67e-30
37	472	49.4	124.7	US-04-478	Sequence 63, Application	7.05e-30
38	471	49.3	123.13	PCT-US95-0	Sequence 11, Application	7.05e-30
39	471	49.3	142.13	PCT-US93-1	Sequence 17, Application	7.05e-30
40	468	49.0	117.11	PCT-US93-1	Sequence 7, Application	1.25e-29
41	468	49.0	119.13	PCT-US95-0	Sequence 12, Application	1.25e-29
42	465	48.5	119.13	PCT-US95-0	Sequence 10, Application	2.32e-29
43	462	48.3	116.6	US-07-634	Sequence 5, Application	3.97e-29
44	462	48.3	116.6	US-08-477	Sequence 5, Application	3.97e-29
45	462	48.3	135.6	US-07-634	Sequence 19, Application	3.97e-29

ALIGNMENTS

RESULT 1
ID PCT-US95-01219-45 STANDARD: PPT: 129 AA.
XX
AC xxxxxx
DT 01-JAN-1900
DE Sequence 45, Application PCT/US9501219.
XX
Sequence 45, Application PCT/US9501219
GENERAL INFORMATION:
APPLICANT: Begg, Mary M.
APPLICANT: Legier, Olivier J.
APPLICANT: Saidanah, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leptocyte
TITLE OF INVENTION: Adhesion Molecule VLA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.025
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01219
FILING DATE: 25-JAN-1995
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/266,269
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:

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CC LENGTH: 129 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 129 AA: 13930 MW: 96169 CN:

Query Match 63.5%; Score 607, DB 13; Length 129;
Best Local Similarity 67.2%; Pred. No. 2,43e-41;
Matches 90; Conservative 22; Mismatches 15; Indels 7; Gaps 7;

Db 1 QVOLV-OSGAEVKPGASVVKSCASGYFTFTSYAISWVRQAPGQGLEWMG-WINPYGND 58
QY : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVOLLEQSGAEVKKPGSSVKVSCKASGTFSGHVTITVRQAPGQGLEWMGESIPFGSAN 60
QY : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 59 -T-NYAQKFGQGRVITADTSTSTAYMELSLRSDETTAVYICARAPG-YGSGGGCYRGDYX 115
QY : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 YAQNYAQKFRDVRVSIADSTSTFIELSLNLSRSDTTAVYICARDPPRYCSAGRCYPG-F 118
QY : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 116 FDYWGQGTLLTVSS 129
QY : ||||| |||||
Db 119 FQWGGQTLTVSS 132
QY : ||||| |||||

RESULT 2
ID PCT-US93-10555-13 STANDARD: PRT: 120 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 13, Application PC/TUS9310555.
XX
CC Sequence 13, Application PC/TUS9310555
CC GENERAL INFORMATION:
CC APPLICANT: SILVERMAN, GREGG J.
CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
CC THROUGH
CC ATES
CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
CC TITLE OF INVENTION: THEREOF
CC NUMBER OF SEQUENCES: 51
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Jubas & Lubitz
CC STREET: 1880 Century Park East - Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067
CC COMPUTER READABLE FORM.
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/10555
CC FILING DATE: 29-OCT-1993
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Howells, Stacy L.
CC REGISTRATION NUMBER: 34,842
CC REFERENCE/DOCKET NUMBER: FD-2630
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 120 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide

US-08-844-215-1-rai
IMMEDIATE SOURCE:
CC CLONE: KAS
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..120
CC SEQUENCE 120 AA: 13008 MW: 78865 CN:

Query Match 58.5%; Score 550, DB 11; Length 120;
Best Local Similarity 68.7%; Pred. No. 2,79e-37;
Matches 90; Conservative 16; Mismatches 14; Indels 11; Gaps 7;

Db 1 VHLV-OSGAEVKPGSSVKVSCKASGTFSSVAISWVRQAPGQGLEWMGSIPIFG--Q 56
QY : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 VQLLESGAEVRRPGSSVKVSCKASGTFSGHVTITVRQAPGQGLFMM-FSIPFGSAN 61
QY : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 57 A-NYAQKFGQGRVITADSTNTAYMELSLRSDDTAMVYICAKPG--YDYGKPF-IF--- 109
QY : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 AQNYAQKFRDVRVSIADSTSTFIELSLNLSRSDTAVYICARPPRYCSAGRCYPGFG 121
QY : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 110 WGQGTLLTVSS 120
QY : ||||| |||||
Db 122 WGQGTLLTVSS 132
QY : ||||| |||||

RESULT 3
ID PCT-US93-10555-12 STANDARD: PRT: 120 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 12, Application PC/TUS9310555.
XX
CC Sequence 12, Application PC/TUS9310555
CC GENERAL INFORMATION:
CC APPLICANT: SILVERMAN, GREGG J.
CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
CC THROUGH
CC ATES
CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
CC TITLE OF INVENTION: THEREOF
CC NUMBER OF SEQUENCES: 51
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Jubas & Lubitz
CC STREET: 1880 Century Park East - Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067
CC COMPUTER READABLE FORM.
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/10555
CC FILING DATE: 29-OCT-1993
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Howells, Stacy L.
CC REGISTRATION NUMBER: 34,842
CC REFERENCE/DOCKET NUMBER: FD-2630
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 120 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide

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CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/053,131
CC FILING DATE: 26-APR-1993
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/990,860
CC FILING DATE: 16-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/910,279
CC FILING DATE: 17-DEC-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/853,408
CC FILING DATE: 18-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-9-3
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-326-2400
CC TELEFAX: 415-326-2422
CC INFORMATION FOR SEQ ID NO: 63:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 102 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 102 AA: 10940 MW: 55761 CN:

Query Match 53.9%; Score 515; DB 7; Length 102;
Best Local Similarity 74.8%; Pred. No. 1,42e-33;
Matches 77; Conservative 13; Mismatches 8; Indels 5; Gaps 61

Db 5 QVQLV-QSGAEVKKPGSSVKVSCKASGTFSTPSYALISWVQAPQGQGLEWVGPIILG-I- 61
QY 1 EVQLLEQSGAEVKKPGSSVKVSCKASGTFSTPSYALISWVQAPQGQGLEWVGPIILG-I- 60
Db 62 -A-NVAQKFGQGVTTITAKSTSTAYMELSLPSEDTAVYYCAR 102
QY 61 YACNYAQKRDVSVIIADESTSTFIELSNLESDTAVYYCAR 103

RESULT 9
ID PCT-US95-00067-2 STANDARD: PFT: 122 AA
XX xxxxxx
XX 01-JAN-1900
DE Sequence 2, Application PC/TUS9500067.
CC GENERAL INFORMATION:
CC APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
CC TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HERPES
CC TITLE OF INVENTION: SIMPLEX VIRUS AND METHODS THEREFOR
CC NUMBER OF SEQUENCES: 25
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Tubes & Lubitz
CC STREET: 1800 Century Park East, Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk

CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/053,131
CC FILING DATE: 26-APR-1993
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/990,860
CC FILING DATE: 16-DEC-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/910,279
CC FILING DATE: 17-DEC-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/853,408
CC FILING DATE: 18-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Haile, Ph.D., Lisa A.
CC REGISTRATION NUMBER: 38,347
CC REFERENCE/DOCKET NUMBER: FD-322q
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 122 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: FARHSV 8
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1-122
CC SEQUENCE 122 AA: 12966 MW: 86647 CN:

Query Match 53.9%; Score 515; DB 13; Length 122;
Best Local Similarity 63.3%; Pred. No. 1,42e-33;
Matches 91; Conservative 20; Mismatches 21; Indels 6; Gaps 3;

Db 1 LEQSGAEVKKPGSSVKVSCKASGTFSSYAINWVQAPQGQGLEWVGGLPIPTTNYAQ- 59
QY 5 LEQSGAEVKKPGSSVKVSCKASGTFSSYAINWVQAPQGQGLEWVGGLPIPTTNYAQ- 54
Db 60 ---KFDPTITADVSTSTAYMQLSLTYEDTAMYYCAP-VA-YMLEPTVTAGGLVWQO 114
QY 60 YAKKPPQSVIIADESTSTFIELSNLESDTAVYYCAPDFEYVSAGPCYPTFFQWQO 124
Db 115 GITVTVAS 122
QY 125 GITVTVSS 132

RESULT 10
ID PCT-US93-11612-8 STANDARD: PFT: 121 AA
XX xxxxxx
XX 01-JAN-1900
DE Sequence 8, Application PC/TUS9311612.
CC GENERAL INFORMATION:
CC APPLICANT: Co. Man Sung
CC TITLE OF INVENTION: Humanized Antibodies Reactive with
CC TITLE OF INVENTION: L-selectin
CC NUMBEP OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:

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US-08-844-215-1-rai

Thu Feb 26 07:03:34 1998

CC APPLICATION NUMBER: PCT/US93/11612
 CC FILING DATE:
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA: US 07/983,946
 CC FILING DATE: 01-DEC-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 11823-22
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-326-2400
 CC TELEFAX: 415-326-2422
 CC INFORMATION FOR SEQ ID NO: 8:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 121 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 121 AA: 13661 MW: 87993 CN;
 SO
 Query Match 53.6%; Score 512; DB 11; Length 121;
 Best Local Similarity 61.4%; Pred. No. 2,54e-33;
 Matches 81; Conservative 24; Mismatches 16; Indels 11; Gaps 7;
 Db 1 QVQLV-QSGAEVKKFGSSVKVSKASGYTFTSYVMHWRQAPGQGLEWIG--Y-IYFND 56
 QY 1 EVQLLEQSGAEVRRKPGSSVKVSKASGGTFTSGHVTITWRQAPGQGLEWIGESIPFGSAN 60
 Db 57 -GTKYNEKFGRTVITSDSTINAYMELSLRSEDATVYYCAREE--Y--GN-VYRYEV 109
 QY 61 YAQNYAQKFRDVSITIADESTSTFIELSLNRSDDTAVYYCARDPPRYCSAGRCYPGFFQ 120
 Db 110 DWGGTGLTVSS 121
 QY 121 QWGGTGLTVSS 132
 RESULT 11
 ID PCT-US93-11612-12 STANDARD: PRT: 140 AA.
 XX
 AC xxxxxx
 DT 01-JAN-1900
 XX
 DE Sequence 12, Application PC/TUS9311612.
 CC
 CC Sequence 12, Application PC/TUS9311612
 CC GENERAL INFORMATION:
 CC APPLICANT: Co. Man Supg
 CC TITLE OF INVENTION: Humanized Antibodies Reactive with
 CC TITLE OF INVENTION: L-Selectin
 CC NUMBER OF SEQUENCES: 12
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend Khourie and Crew
 CC STREET: One Market Plaza, Steuart Tower, Suite 2000
 CC CITY: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC OPERATING SYSTEM: IBM PC compatible
 CC SOFTWARE: Patent in Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/11612
 CC FILING DATE:
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/983,946
 CC FILING DATE: 01-DEC-1992

CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 11823-22
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-326-2400
 CC TELEFAX: 415-326-2422
 CC INFORMATION FOR SEQ ID NO: 12:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 140 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 140 AA: 15650 MW: 117746 CN;
 SQ
 Query Match 53.6%; Score 512; DB 11; Length 140;
 Best Local Similarity 61.4%; Pred. No. 2,54e-33;
 Matches 81; Conservative 24; Mismatches 16; Indels 11; Gaps 7;
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 QY 1 EVQLLEQSGAEVRRKPGSSVKVSKASGGTFTSGHVTITWRQAPGQGLEWIGESIPFGSAN 60
 Db 76 -GTKYNEKFGRTVITSDSTINAYMELSLRSEDATVYYCAREE--Y--GN-VYRYEV 128
 QY 61 YAQNYAQKFRDVSITIADESTSTFIELSLNRSDDTAVYYCARDPPRYCSAGRCYPGFFQ 120
 Db 129 VWGGTGLTVSS 140
 QY 121 QWGGTGLTVSS 132
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 ID US-08-477-728-4 STANDARD: PRT: 117 AA.
 XX
 AC xxxxxx
 DT 01-JAN-1900
 XX
 DE Sequence 4, Application US/08477728.
 CC
 CC Sequence 4, Application US/08477728
 CC Patent No. 585089
 CC GENERAL INFORMATION:
 CC APPLICANT: QUEEN, Cary L.
 CC APPLICANT: SCHNEIDER, William P.
 CC APPLICANT: SELICK, Harold E.
 CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 CC NUMBER OF SEQUENCES: 113
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend and Crew LLP
 CC STREET: Two Embarcadero Center, 8th Floor
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94111
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC OPERATING SYSTEM: IBM PC compatible
 CC SOFTWARE: Patent in Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/477,728
 CC FILING DATE: 07-JUN-1995
 CC CLASSIFICATION: 424
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/634,278
 CC FILING DATE: 19-DEC-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/590,274
 CC FILING DATE: 28-SEP-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/418,252

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CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/500,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,323
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 15:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: NO
CC FEATURE:
CC NAME/KEY: protein
CC LOCATION: 1..117
CC OTHER INFORMATION: /note= "Eu heavy chain amino acid
CC OTHER INFORMATION: sequence "
CC SEQUENCE 117 AA; 12472 MW; 77871 CN;

Query Match 51.2%; Score 489; DB 6; Length 117;
Best/Local Similarity 70.6%; Pred. No. 2.17e-31;
Matches 72; Conservative 16; Mismatches 9; Indels 5. Gaps

Db 1 QVQIV-QSCAEYKPGSSVKYSKASGSIETSRSAIHWKQAPQGGIFWVGIVPMKPPN 59
Cy 1 EVALLLEISAEYKPGSSVKYSKASGSIETSGHVIHWKQAPQGGIETWVGSIPIFGSAN 60

Db 60 YAQ----KFGVTTADESTNAYMELSLRSDEAFYCA 97
Cy 61 YAQYAKQFDRVYSIADESTSTFIELSNLRSDTAVYCA 102

RESULT 14
ID US-07-634-278-15 STANDARD; FRT: 117 AA.
XX XXXXXX
XX 01-JAN-1900
DE Sequence 15, Application US/07634278.
XX
CC Sequence 15, Application: US/07634278
CC Patent No. 5530101
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLF, Nicholas F.
CC APPLICANT: GOELINGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: Townsend and Townsend Kourie and Crew
CC STREET: 379 Lytton Avenue
CC City: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301

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CORRESPONDENCE ADDRESS:
ATTENESSE: Townsend and Townsend Kourie and Clew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 42A
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE: 117 AA; 12472 MW; 77871 CN;

Query Match 51.2%; Score 489; DB 6; Length 11
Best Local Similarity 70.6%; Pred. No. 2,17e-31;
Matches 72; Conservative 16; Mismatches 9; Indels

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6U YAQ-----KPGRVILTADESTNTAYMELSLSRSDTAFTCA 97
111 YAQYQAFKRVISLIADESTSTFIELSNLKSUDTAFTCA 102
61 YAQYQAFKRVISLIADESTSTFIELSNLKSUDTAFTCA 102

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CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/634,278
CC FILING DATE: 19-DEC-1990
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PROIP APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO.: 15:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: NO
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..117
CC OTHER INFORMATION: /note= "Eu heavy chain amino acid
CC OTHER INFORMATION: sequence."
CC SEQUENCE 117 AA; 12472 MW; 77871 CN;

Query Match 51.2%; Score 489; DB 6; Length 117;
Best Local Similarity 70.6%; Pied.No. 2.17e-31;
Matches 72; Conservative 16; Mismatches 9; Indels 5; Gaps 2;

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Qy 1 EVQLLESGSFAEKVPKPGSSVKVSKASGGTFSGHVITWVRQAPGGGLEWMGESIPFGSAN 60
Ddb 60 QVQLV----KFOGRVTITADESTNTAYMELSSLRSEDTAFYFCA 97
Qy 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
111 111 111 111 111 111 111 111 111 111 111 111 111 111
Qy 61 YAQYAQKFKFPDPVSITADESTSTFIELSNLRSDDTAVYYCA 102

RESULT 15
ID US-07-634-278-72 STANDARD; PRT; 117 AA.
XX XXXXXX
DT 01-JAN-1900
DE Sequence 72, Application US/07634278.
XX
CC Sequence 72, Application US/07634278
CC Patent No. 5530101
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO. Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELINGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
```

WQREH
(TX)

Release 2.1D John F. Collins, Biocomputing Research Unit
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Distribution rights by Intelligentics, Inc.
MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:03:36 1998. MaxPat: time 8.15 Sec: 0.01s
Tabular output not generated
Title: >US-08-844-215-1
Description: (1-132) from US08844215.pcp
Perfect Score: 956
Sequence: 1 EVQLLEQSGAEVPRKPGSSVK... PCYPGFPQWGGTLTVSS 132

Scoring table: PAM 150
Gap 11
Searched: 95051 seqs, 30469580 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: p1r53
1:ann1 2:ann2 3:ann3 4:ann4 5:ann5 6:ann6 7:ann7 8:ann8 9:ann9 10:ann10 11:ann11 12:ann12 13:ann13 14:ann14 15:ann15 16:ann16 17:ann17 18:uncrev

Statistics: Mean 41.620; Variance 105.958; scale 0.393
Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	DR	ID	Description	Pred. No.
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2	584	61.1	126	7	PH0952	Ig heavy chain V reg	1.21e-71
3	579	60.6	129	7	A33548	Ig heavy chain V-1 r	7.54e-71
4	577	60.4	127	7	PH0955	Ig heavy chain V reg	1.57e-70
5	575	60.1	126	7	B33548	Ig heavy chain V-1 r	3.27e-70
6	567	59.3	160	7	PI0105	anti-PP2 erythrocyte	6.10e-69
7	566	59.2	120	7	PH0952	Ig heavy chain V reg	8.80e-69
8	560	58.6	135	7	PH0953	Ig heavy chain V reg	7.90e-68
9	559	58.5	132	7	PH0954	Ig heavy chain V reg	1.14e-67
10	551	57.6	129	7	S36560	Ig heavy chain V reg	2.11e-66
11	549	57.4	126	7	S36561	Ig heavy chain V reg	4.38e-66
12	545	57.1	121	7	A49590	Ig heavy chain V reg	1.31e-65
13	545	57.1	132	7	S46304	Ig heavy chain V reg	1.31e-65
14	545	57.0	133	7	C33548	Ig heavy chain V-1 r	1.89e-65
15	545	57.0	627	7	S14683	Ig mu chain precursor	1.89e-65
16	544	56.9	126	7	PH0950	Ig heavy chain V reg	2.72e-65
17	542	56.7	126	7	PH0959	Ig heavy chain V reg	5.64e-65
18	542	56.7	122	7	PH0958	Ig heavy chain V reg	5.64e-65
19	538	56.3	119	7	PH0961	Ig heavy chain V reg	2.42e-64
20	538	56.3	123	7	D23549	Ig heavy chain V-1 r	2.42e-64

21	537	56.2	98	7	S26915 Ig heavy chain V reg	3.49e-64
22	537	56.2	116	7	S31698 Ig heavy chain V reg	3.49e-64
23	537	56.2	123	7	S44108 Ig heavy chain V-1 r	3.49e-64
24	535	56.0	98	7	S24680 Ig heavy chain V-1 r	7.23e-64
25	535	56.0	119	7	S44105 Ig heavy chain V-1 r	7.23e-64
26	531	55.5	113	7	PH1563 Ig heavy chain V reg	3.10e-63
27	527	55.1	122	7	B49590 Ig heavy chain V reg	1.32e-62
28	518	54.3	125	7	B32374 Ig heavy chain V reg	2.51e-61
29	515	53.9	98	7	S45463 Ig heavy chain V reg	1.04e-60
30	515	53.9	129	7	S46393 Ig heavy chain V reg	1.04e-60
31	513	53.7	122	7	C49590 Ig heavy chain V reg	2.15e-60
32	510	53.3	131	7	S21924 Ig heavy chain V reg	6.41e-60
33	505	52.8	97	7	PH0870 Ig heavy chain V reg	3.93e-59
34	503	52.6	124	7	S19665 Ig heavy chain V reg	8.11e-59
35	499	52.2	122	7	S36271 Ig heavy chain V reg	2.46e-58
36	494	51.7	148	7	S29237 Ig heavy chain V reg	2.11e-57
37	490	51.3	108	7	PH1684 Ig heavy chain V reg	8.98e-57
38	489	51.2	127	2	GIRUEV Ig heavy chain V-1 r	1.29e-56
39	487	50.9	142	7	A32483 Ig heavy chain V reg	2.65e-56
40	484	50.6	136	7	PH0535 Ig heavy chain V reg	2.65e-56
41	483	50.5	116	7	S31667 Ig heavy chain V reg	1.13e-55
42	481	50.3	98	7	A30523 Ig heavy chain V-1 r	2.32e-55
43	475	49.7	109	7	PH1671 Ig heavy chain V reg	2.02e-54
44	475	49.7	119	7	F49590 Ig heavy chain V reg	2.02e-54
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ALIGNMENTS

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ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
ACCESSIONS PH0957
REFERENCE PH0952
#authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J Exp Med (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MIM:2202880
#accession PH0957
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 1-125 #label MAP
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
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51-67 #region framework 2\
68-98 #region complementarity-determining 2\
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DB	60	qag---kfgrvttidestntarmolsslrtsodtavyvcardg---csqgscvfwf	112
Qy	61	YAOYNAKKEKDFPVSLIAETSTSTSFIELSNLPSHQAAYVYCAAPPPYCAAGVYP	119
DB	113	dwagglvtvss	125
Qy	122	qewgglvtvss	122

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TITLE Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
ACCESSIONS PH0952
REFERENCE Martin, T.J.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#authors J. Exp. Med. (1992) 175:983-991
#journal Evidence for somatic selection of natural autoantibodies.
#title #cross-references MUID:92202880
#accession PH0952
#molecule_type DNA
#status nucleic acid sequence not shown
#residues 1-129 ##label MAR
#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 1-30
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15-98 #domain immunoglobulin homology #label IMM
31-35 #region complementarity-determining 1\
36-50 #region framework 2\
51-67 #region complementarity-determining 2\
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99-116 #region complementarity-determining 3
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Best Local Similarity 68.7%; Pred No. 7,54e-71;
Matches 92; Conservative 16; Mismatches 19; Indels 7; Gaps 3;

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 1-30
1-30 #region framework 1\
15-98 #domain immunoglobulin homology #label IMM
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36-50 #region framework 2\
51-67 #region complementarity-determining 2\
68-98 #region framework 3\
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SUMMARY #length 129 #molecular_weight 13932 #checksum 4075
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Best Local Similarity 68.7%; Pred No. 7,54e-71;
Matches 92; Conservative 16; Mismatches 19; Indels 7; Gaps 3;

Db 1 qvqlv-qsgaevkpgssvkscasgtfssyalswvrgpqqqlwmqgllpifgtan 59
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#region framework 1\
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#region framework 2\
#region complementarity-determining 2\
#region framework 3\
#region complementarity-determining 3
SUMMARY #length 129 #molecular_weight 13932 #checksum 4075
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Best Local Similarity 68.7%; Pred No. 7,54e-71;
Matches 92; Conservative 16; Mismatches 19; Indels 7; Gaps 3;

Db 60 yaq---kfgrvtitadeststymelsslrscdtavvyrcarprrlladvllwfgelse 115
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Best Local Similarity 68.7%; Pred No. 7,54e-71;
Matches 92; Conservative 16; Mismatches 19; Indels 7; Gaps 3;

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#domain immunoglobulin homology #label IMM
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#region framework 2\
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#region framework 3\
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Best Local Similarity 68.7%; Pred No. 7,54e-71;
Matches 92; Conservative 16; Mismatches 19; Indels 7; Gaps 3;

RESULT 4
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TITLE Ig heavy chain V region (G6+ CLL-AND) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
ACCESSIONS PH0955
REFERENCE Martin, T.J.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#authors J. Exp. Med. (1992) 175:983-991
#journal Evidence for somatic selection of natural autoantibodies.
#title #cross-references MUID:92202880
#accession PH0955
#molecule_type DNA
#status nucleic acid sequence not shown
#residues 1-127 ##label MAR
#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
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31-35 #region complementarity-determining 1\
36-50 #region framework 2\
51-67 #region complementarity-determining 2\
68-98 #region framework 3\
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Best Local Similarity 66.9%; Pred No. 1,57e-70;
Matches 89; Conservative 19; Mismatches 18; Indels 7; Gaps 4;

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 1-30
1-30 #region framework 1\
15-98 #domain immunoglobulin homology #label IMM
31-35 #region complementarity-determining 1\
36-50 #region framework 2\
51-67 #region complementarity-determining 2\
68-98 #region framework 3\
99-115 #region complementarity-determining 3
SUMMARY #length 127 #checksum 6297
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Best Local Similarity 66.9%; Pred No. 1,57e-70;
Matches 89; Conservative 19; Mismatches 18; Indels 7; Gaps 4;

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#region complementarity-determining 1\
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#region framework 3\
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Best Local Similarity 66.9%; Pred No. 1,57e-70;
Matches 89; Conservative 19; Mismatches 18; Indels 7; Gaps 4;

Db 60 yaq---kfgrvtitadeststymelsslrscdtavvyrcarprrlladvllwfgelse 114
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#domain immunoglobulin homology #label IMM
#region complementarity-determining 1\
#region framework 2\
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SUMMARY #length 127 #checksum 6297
Query Match 60.4%; Score 577; DB 7; Length 127;
Best Local Similarity 66.9%; Pred No. 1,57e-70;
Matches 89; Conservative 19; Mismatches 18; Indels 7; Gaps 4;

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#domain immunoglobulin homology #label IMM
#region complementarity-determining 1\
#region framework 2\
#region complementarity-determining 2\
#region framework 3\
#region complementarity-determining 3
SUMMARY #length 127 #checksum 6297
Query Match 60.4%; Score 577; DB 7; Length 127;
Best Local Similarity 66.9%; Pred No. 1,57e-70;
Matches 89; Conservative 19; Mismatches 18; Indels 7; Gaps 4;

3
RESULT 3
ENTRY A33548 #type complete
TITLE Ig heavy chain V-1 region (NEI) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
ACCESSIONS A33548; PH0956
REFERENCE Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chan, P.P.; Carson, D.A.
#authors Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
#journal Developmentally restricted immunoglobulin heavy chain
#title variable region gene expressed at high frequency in chronic lymphocytic leukemia.
#cross-references MUID:89345575
#accession A33548
#molecule_type mRNA
#status preliminary; not compared with conceptual translation
#residues 1-129 ##label KIR
#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 1-30
1-30 #region framework 1\
15-98 #domain immunoglobulin homology #label IMM
31-35 #region complementarity-determining 1\
36-50 #region framework 2\
51-67 #region complementarity-determining 2\
68-98 #region framework 3\
99-116 #region complementarity-determining 3
SUMMARY #length 129 #molecular_weight 13932 #checksum 4075
Query Match 61.1%; Score 584; DB 7; Length 128;
Best Local Similarity 67.9%; Pred No. 1,21e-71;
Matches 91; Conservative 18; Mismatches 17; Indels 8; Gaps 5;

Db 1 qvqlv-qsgaevkpgssvkscasgtfssyalswvrgpqqqlwmqgllpifgtan 59
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1 EVQLLEQSGAEVKKPKSSVKVSKASGGTFSGHVTWVROAPGQGLEWMGESIPFGSAN 60
#region framework 1\
#domain immunoglobulin homology #label IMM
#region complementarity-determining 1\
#region framework 2\
#region complementarity-determining 2\
#region framework 3\
#region complementarity-determining 3
SUMMARY #length 128 #checksum 3537
Query Match 61.1%; Score 584; DB 7; Length 128;
Best Local Similarity 67.9%; Pred No. 1,21e-71;
Matches 91; Conservative 18; Mismatches 17; Indels 8; Gaps 5;

Db 60 yaq---kfgrvtitadeststymelsslrscdtavvyrcargnydiwgsyrndaf 115
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 YAQNYAQKFRDRVSIADSTSTFIELSNLRSDDTAVVYCARPPRYCSAGRCYPGF 118
#region framework 1\
#domain immunoglobulin homology #label IMM
#region complementarity-determining 1\
#region framework 2\
#region complementarity-determining 2\
#region framework 3\
#region complementarity-determining 3
SUMMARY #length 128 #checksum 3537
Query Match 61.1%; Score 584; DB 7; Length 128;
Best Local Similarity 67.9%; Pred No. 1,21e-71;
Matches 91; Conservative 18; Mismatches 17; Indels 8; Gaps 5;

Db 116 -diwqggtlvtvss 128
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 119 FOQWGGTILTVSS 132
#region framework 1\
#domain immunoglobulin homology #label IMM
#region complementarity-determining 1\
#region framework 2\
#region complementarity-determining 2\
#region framework 3\
#region complementarity-determining 3
SUMMARY #length 128 #checksum 3537
Query Match 61.1%; Score 584; DB 7; Length 128;
Best Local Similarity 67.9%; Pred No. 1,21e-71;
Matches 91; Conservative 18; Mismatches 17; Indels 8; Gaps 5;
```



```

RESULT      5
ENTRY
TITLE      B33548      #type complete
ORGANISM    Ig heavy chain V-1 region (AND) - human
DATE        #formal_name Homo sapiens #common_name man
            17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
            16-Aug-1996
ACCESSIONS  B33548
REFERENCE    Kippes, T.J., Tomhave, E., Pratt, L.F., Daffy, S., Chen, F.P.,
            Carson, D.A.
            Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
            Developmentally restricted immunoglobulin heavy chain
            variable region gene expressed at high frequency in chronic
            lymphocytic leukemia.
            #cross-references MUID:89345575
            #accession B33548
            #status preliminary; nucleic acid sequence not shown; not
            compared with conceptual translation
            ##molecule_type DNA
            ##residues 1-126 #label KIP
            ##experimental_source the sequence was determined from the
            differentiated gene
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98
SUMMARY
Query Match 50.4% Score 575; DB 7; Length 126;
Best Local Similarity 57.4%; Pred. No. 3 27e-70;
Matches 89; Conservative 18; Mismatches 19; Indels 6; Gaps 3;
Db 1 gqqlv-qsgaevkpgssvskasgdtfssyaiswvraqpagglewag-wisv-y-nod 59
QY 1 EVQLLEQSGAEVRKPGSSVSKASGGIFSGHVIWVRQAPGGGLEWGESIPFGSAN 60
Db 60 yag----kfgqvttadststststststststststststststststststst 114
QY 61 YAGNYAKKRPDPVSIINAEISTSTFIELSNLPSCDTAVYVCARPPPYCSAGPCYPGPFQ 120
Db 115 vwqlgtttvss 126
QY 121 QWGGTLTVSS 132
RESULT      6
ENTRY
TITLE      PL0105      #type fragment
ORGANISM    anti-PP2 erythrocyte autoantibody heavy chain precursor
            human (fragment)
DATE        #formal_name Homo sapiens #common_name man
            31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
            26-Apr-1996
ACCESSIONS  PL0105
REFERENCE    Silberstein, L.E.; Litwin, S.; Carmack, C.E.
            J. Exp. Med. (1989) 169:1631-1643
            Pelatich of variable region genes expressed by a human B
            cell lymphoma secreting pathologic anti-pp-2 erythrocyte
            autoantibodies.
            #cross-references MUID:89235583
            #accession PL0105
            ##molecule_type mRNA
            ##residues 1-160 #label SIL
            ##note the authors translated the codon GAC for residues 108
            and 109 as Glu
COMMENT      The antibody is one of the cold agglutinins that preferentially
            bind red blood cell membrane antigens at low temperature, causing
            cold agglutinin disease (CAD).
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS autoantibody; hemagglutinin
FEATURE

```

```

1-19
34-117
49-54
69-84
118-131
132-144
145-160
SUMMARY      #length 160 #checksum 3900
Query Match 59.4% Score 567; DB 7; Length 160;
Best Local Similarity 64.4%; Pred. No. 6 10e-69;
Matches 85; Conservative 24; Mismatches 16; Indels 7; Gaps 7;
Db 20 gqqlv-qsgaevkpgssvskasgdtfssyaiswvraqpagglewag-wisv-y-nod 75
QY 1 EVQLLEQSGAEVRKPGSSVSKASGGIFSGHVIWVRQAPGGGLEWGESIPFGSAN 60
Db 77 -t-nyagqlgrvtmttdststststststststststststststststststst 132
QY 61 YAGNYAKKRPDPVSIINAEISTSTFIELSNLPSCDTAVYVCARPPPYCSAGPCYPGPFQ 120
Db 133 ywgggtltvss 144
QY 121 QWGGTLTVSS 132
RESULT      7
ENTRY
TITLE      PH0962      #type fragment
ORGANISM    Ig heavy chain V region (G6+ T-142) - human (fragment)
            #formal_name Homo sapiens #common_name man
            17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
            16-Aug-1996
ACCESSIONS  PH0962
REFERENCE    Martin, T., Daffy, S.F., Carson, D.A., Kippes, T.J.
            J. Exp. Med. (1992) 175:983-991
            Evidence for somatic selection of natural autoantibodies.
            #cross-references MUID:9202880
            #accession PH0962
            #status nucleic acid sequence not shown
            ##molecule_type DNA
            ##residues 1-120 #label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-30
15-98
31-35
36-50
51-67
68-98
99-108
SUMMARY      #length 120 #checksum 5559
Query Match 59.4% Score 566; DB 7; Length 120;
Best Local Similarity 72.0%; Pred. No. 8.80e-69;
Matches 95; Conservative 14; Mismatches 11; Indels 12; Gaps 5;
Db 1 gqqlv-qsgaevkpgssvskasgdtfssyaiswvraqpagglewag-wisv-y-nod 59
QY 1 EVQLLEQSGAEVRKPGSSVSKASGGIFSGHVIWVRQAPGGGLEWGESIPFGSAN 60
Db 60 yag -- kfgqvttadststststststststststststststststststst 109
QY 61 YAGNYAKKRPDPVSIINAEISTSTFIELSNLPSCDTAVYVCARPPPYCSAGPCYPGPFQ 120
Db 109 ywgggtltvss 120
QY 121 QWGGTLTVSS 132
RESULT      8
ENTRY
TITLE      PH0953      #type fragment

```

Thu Feb 26 07:03:36 1998

```

TITLE
ORGANISM
DATE
Iq heavy chain V region (G6+ CLL-SiC) - human (fragment)
#formal_name Homo sapiens #common_name man
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
PH0953
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:92202880
#accession
PH0953
#status
#molecule_type DNA
#residues
1-135 #label MAR
CLASSIFICATION
#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS
heterotetramer; immunoglobulin
FEATURE
1-30
15-98
31-35
36-50
51-67
68-98
99-123
#length 135 #checksum 2318
SUMMARY
Query Match 58.6%; Score 560; DB 7; Length 135;
Best Local Similarity 72.4%; Pred. No. 7.90e-68;
Matches 84; Conservative 16; Mismatches 8; Indels 8; Gaps 4;
Db 1 qvqlv-qsgaevkpgssvskvscasggtfssyaiswvrqapgggvmgiiipigtan 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLEQSGAEVRFGSSVKSKASGTFSGHVTWVRQAPGQGLEWMGESIPIFGSAN 60
16-Aug-1996
PH0954
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:92202880
#accession
PH0954
#status
#molecule_type DNA
#residues
1-132 #label MAR
CLASSIFICATION
#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS
heterotetramer; immunoglobulin
FEATURE
1-30
15-98
31-35
36-50
51-67
68-98
99-120
#length 132 #checksum 9232
SUMMARY
Query Match 58.5%; Score 559; DB 7; Length 132;
Best Local Similarity 66.4%; Pred. No. 1.14e-67;
Matches 91; Conservative 18; Mismatches 18; Indels 10; Gaps 5;
Db 1 qvqlv-qsgaevkpgssvskvscasggtfssyaiswvrqapgggvmgiiipigtan 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

QY 1 EVQLLEQSGAEVRFGSSVKSKASGTFSGHVTWVRQAPGQGLEWMGESIPIFGSAN 60
Db 60 yaq----kfggrvtideststymelsslrstdtavvycaiphasidifwsqyyfyy 115
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YAQNYAQKFRDRVSLIADESTSTFIELNLSRSDDTAVVYCARDPPRYCSAGRCYP 119
16-Aug-1996
PH0952
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:92202880
#accession
PH0952
#status
#molecule_type DNA
#residues
1-135 #label MAR
CLASSIFICATION
#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS
heterotetramer; immunoglobulin
FEATURE
1-30
15-98
31-35
36-50
51-67
68-98
99-123
#length 135 #checksum 2318
SUMMARY
Query Match 58.6%; Score 560; DB 7; Length 135;
Best Local Similarity 72.4%; Pred. No. 7.90e-68;
Matches 84; Conservative 16; Mismatches 8; Indels 8; Gaps 4;
Db 1 qvqlv-qsgaevkpgssvskvscasggtfssyaiswvrqapgggvmgiiipigtan 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLEQSGAEVRFGSSVKSKASGTFSGHVTWVRQAPGQGLEWMGESIPIFGSAN 60
16-Aug-1996
PH0954
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:92202880
#accession
PH0954
#status
#molecule_type DNA
#residues
1-132 #label MAR
CLASSIFICATION
#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS
heterotetramer; immunoglobulin
FEATURE
1-30
15-98
31-35
36-50
51-67
68-98
99-120
#length 132 #checksum 9232
SUMMARY
Query Match 58.5%; Score 559; DB 7; Length 132;
Best Local Similarity 66.4%; Pred. No. 1.14e-67;
Matches 91; Conservative 18; Mismatches 18; Indels 10; Gaps 5;
Db 1 qvqlv-qsgaevkpgssvskvscasggtfssyaiswvrqapgggvmgiiipigtan 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

##molecule_type mRNA
##residues 1-116 ##label GRI
##cross-references EMBL:Z18841
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98 #domain immunoglobulin homology #label IMM
SUMMARY
#length 116 #checksum 7971

Query Match 57.48; Score 549; DB 7; Length 116;
Best Local Similarity 74.38; Pred. No. 4.39e-66;
Matches 81; Conservative 14; Mismatches 9; Indels 6; Gaps 3;

Db 1 qqlv-qsgaevkpgssvkscasggtfssyaisvswrqpqgglewmgglipifgtan 59
QY 1 EVQLLEQSGAEVRFKPGSSVKVSKASGTFSGHVTITWVQAPQGGLWMGESPIFGSAN 60

Db 60 yaq-----kfggrvtitadeststamelsrsdtaavycarglprgy 104
QY 61 YACNVAKKFPDVPVSIADSTSTSFIELSNLSDTAVVYCAPTPP-Y 108

RESULT 12
ENTRY A49590 #type fragment
TITLE Ig heavy chain V region (ACHSV1, clone 15) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
23-May-1997

ACCESSIONS A49590
REFERENCE Burton, R.; Williamson, P. A.; Sanna, P. P.; Bloom, P. E.;
Burton, D.R.
Proc Natl. Acad. Sci. U.S.A. (1994) 91:355-359
Recombinant human Fab to glycoprotein D neutralizes
infectivity and prevents cell-to-cell transmission of
herpes simplex viruses 1 and 2 in vitro.
#cross-references MUID:94105168
#accession A49590
#status preliminary; not compared with conceptual translation
#residues 1-121 ##label BUP
##cross-references NCBI:P141850
##experimental_source bone marrow lymphocytes
##note sequence extracted from NCBI backbone
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
11-94 #domain immunoglobulin homology #label IMM
SUMMARY
#length 121 #checksum 6226

Query Match 57.18; Score 546; DB 7; Length 121;
Best Local Similarity 64.38; Pred. No. 1.31e-65;
Matches 81; Conservative 20; Mismatches 19; Indels 6; Gaps 4;

Db 2 esgaevkpgssvkscasggtfssyaisvswrqpqgglewmgglipifgtan-b-a 57
QY 7 QSGAEVRFKPGSSVKVSKASGTFSGHVTITWVQAPQGGLWMGESPIFGSANTAGNYA 66

Db 58 qkfggrvtitadeststamelsrsdtaavycar-vg-vcstngoslgmdvwgggt 115
QY 57 QKFPVPSIADSTSTSFIELSNLSDTAVVYCAPTPPFCVCSGPCYPCPFQMGQGT 126

Db 116 tvivss 121
QY 127 LVTVSS 132

RESULT 13
ENTRY S46394 #type complete
TITLE Ig heavy chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change
23-May-1997

```

```

ACCESSIONS S46394
REFERENCE Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. (1994) 239:58-78
#journal In vitro assembly of repertoires of antibody chains on the
#title surface of phage by renaturation.
#accession S46394
#status Preliminary
##molecule_type DNA
##residues 1-132 ##label FIG
##cross-references EMBL:Z31681
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98 #domain immunoglobulin homology #label IMM
SUMMARY
#length 132 #molecular_weight 14293 #checksum 7515

Query Match 57.18; Score 546; DB 7; Length 132;
Best Local Similarity 65.08; Pred. No. 1.31e-65;
Matches 89; Conservative 20; Mismatches 18; Indels 10; Gaps 7;

Db 1 qqlv-qsgaevkpgssvkscasggtfssyaisvswrqpqgglewmgglipifgtan 59
QY 1 EVQLLEQSGAEVRFKPGSSVKVSKASGTFSGHVTITWVQAPQGGLWMGESPIFGSAN 60

Db 60 yaq-----kfggrvtitadeststamelsrsdtaavycar-vg-vcstngoslgmdvwgggt 115
QY 61 YACNVAKKFPDVPVSIADSTSTSFIELSNLSDTAVVYCAPTPPFCVCSGPCY-Y-PGF 118

Db 116 tvivss 121
QY 119 F--QQ-WGQGLTVTVSS 132

RESULT 14
ENTRY C33548 #type complete
TITLE Ig heavy chain V-1 region (783) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
16-Aug-1996

ACCESSIONS C33548
REFERENCE Kipps, T. J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.;
Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
Developmentally restricted immunoglobulin heavy chain
variable region gene expressed at high frequency in chronic
lymphocytic leukemia.
#cross-references MUID:89345575
#accession C33548
#status Preliminary; nucleic acid sequence not shown; not
compared with conceptual translation
##molecule_type DNA
##residues 1-133 ##label KIP
##experimental_source differentiated gene
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98 #domain immunoglobulin homology #label IMM
SUMMARY
#length 133 #molecular_weight 14220 #checksum 1289

Query Match 57.08; Score 545; DB 7; Length 133;
Best Local Similarity 66.48; Pred. No. 1.89e-65;
Matches 93; Conservative 20; Mismatches 12; Indels 15; Gaps 9;

Db 1 qqlv-qsgaevkpgssvkscasggtfssyaisvswrqpqgglewmgglipifgtan 59
QY 1 EVQLLEQSGAEVRFKPGSSVKVSKASGTFSGHVTITWVQAPQGGLWMGESPIFGSAN 60

Db 60 yaq-----kfggrvtitadeststamelsrsdtaavycar-vg-vcstngoslgmdvwgggt 113
QY 61 YACNVAKKFPDVPVSIADSTSTSFIELSNLSDTAVVYCAPTPPFCVCSGPCY-Y-G 117

```

Search completed: Tue Feb 24 07:02:57 1998
Job time : 32 secs.

WILEY
***** (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:01:43 1998; MasPar time 5.55 Seconds
Tabular output not generated. 504.423 Million cell updates/sec

Title: >US-08-844-215-1
Description: (1-132) from US08844215.pep
Perfect Score: 956
Sequence: i EVQLLESGAEVSKPKSSVK... PCYPGFFQWGGILVTYSS 132

Scoring table: PAM 150
Gap 11
Searched: 59021 seqs, 21210388 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11
Statistics: Mean 42 359; Variance 75 508; scale 0.561

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred No.
1	489	51	2	5	HV1A_HUMAN	IG HEAVY CHAIN V-I PE 1 226-81
2	445	46	5	5	HV1B_HUMAN	IG HEAVY CHAIN PRECUR 7 546-72
3	440	46	0	5	HV1G_HUMAN	IG HEAVY CHAIN PRECUR 9 656-71
4	427	44	7	5	HV00_MOUSE	IG HEAVY CHAIN V REGI 7 100-68
5	424	44	4	5	HV1C_HUMAN	IG HEAVY CHAIN PRECUR 3 306-67
6	416	43	5	5	HV02_MOUSE	IG HEAVY CHAIN PRECUR 1 906-65
7	412	43	1	5	HV03_MOUSE	IG HEAVY CHAIN V REGI 1 446-64
8	406	42	5	5	HV1E_HUMAN	IG HEAVY CHAIN V-I PE 3 006-63
9	405	42	4	5	HV1F_HUMAN	IG HEAVY CHAIN V-I PE 4 976-63
10	405	42	4	5	HV1K_HUMAN	IG HEAVY CHAIN V-III 4 976-63
11	394	41	2	5	HV01_MOUSE	IG HEAVY CHAIN V REGI 1 276-60
12	394	41	2	5	HV3G_HUMAN	IG HEAVY CHAIN V-III 1 276-60
13	384	40	2	5	HV05_MOUSE	IG HEAVY CHAIN PRECUR 1 946-58
14	383	40	1	5	HV1D_HUMAN	IG HEAVY CHAIN V-I PE 3 216-58
15	378	39	5	5	HV13_MOUSE	IG HEAVY CHAIN V REGI 3 946-57
16	377	39	4	5	HV04_MOUSE	IG HEAVY CHAIN PRECUR 6 506-57
17	377	39	4	5	HV12_MOUSE	IG HEAVY CHAIN V REGI 6 506-57
18	372	38	9	5	HV52_MOUSE	IG HEAVY CHAIN PRECUR 7 946-56
19	368	38	5	5	HV14_MOUSE	IG HEAVY CHAIN PRECUR 5 866-55
20	368	38	5	5	HV51_MOUSE	IG HEAVY CHAIN V REGI 5 866-55
21	367	38	4	5	HV3E_MOUSE	IG HEAVY CHAIN PRECUR 9 666-55
22	365	38	2	5	HV57_MOUSE	IG HEAVY CHAIN PRECUR 2 626-54

22	364	38 1	120	5	HV50_MOUSE	IG HEAVY CHAIN V REGI	4 328-54
24	364	38 1	138	5	HV48_MOUSE	IG HEAVY CHAIN PRECUR	4 328-54
25	361	37 8	142	5	HV01_PAT	IG HEAVY CHAIN PRECUR	1 936-53
26	358	37 4	137	5	HV11_MOUSE	IG HEAVY CHAIN PRECUR	8 586-53
27	357	37 3	122	5	HV3H_HUMAN	IG HEAVY CHAIN V-III	1 416-52
28	356	37 2	119	5	HV3N_HUMAN	IG HEAVY CHAIN V-III	2 226-52
29	356	37 2	120	5	HV1H_HUMAN	IG HEAVY CHAIN V-I PE	2 326-52
30	352	36 8	117	5	HV45_MOUSE	IG HEAVY CHAIN PRECUR	1 706-51
31	350	36 6	117	5	HV09_MOUSE	IG HEAVY CHAIN PRECUR	4 586-51
32	346	36 2	119	5	HV3M_HUMAN	IG HEAVY CHAIN V-III	3 336-50
33	345	36 1	119	5	HV3I_HUMAN	IG HEAVY CHAIN V-III	5 466-50
34	344	36 0	113	5	HV30_MOUSE	IG HEAVY CHAIN V-III	8 966-50
35	344	36 0	115	5	HV32_MOUSE	IG HEAVY CHAIN V-III	8 966-50
36	344	36 0	144	5	HV26_MOUSE	IG HEAVY CHAIN PRECUR	8 966-50
37	341	35 7	113	5	HV28_MOUSE	IG HEAVY CHAIN V-III	3 966-49
38	341	35 7	113	5	HV27_MOUSE	IG HEAVY CHAIN V-III	3 966-49
39	340	35 6	117	5	HV03_CAPAU	IG HEAVY CHAIN PRECUR	6 496-49
40	340	35 6	117	5	HV3C_HUMAN	IG HEAVY CHAIN PRECUR	6 496-49
41	340	35 6	120	5	HV10_MOUSE	IG HEAVY CHAIN PRECUR	6 496-49
42	340	35 6	120	5	HV3E_HUMAN	IG HEAVY CHAIN V-III	6 496-49
43	340	35 6	121	5	HV3J_HUMAN	IG HEAVY CHAIN V-III	6 496-49
44	337	35 3	113	5	HV34_MOUSE	IG HEAVY CHAIN V REGI	2 866-48
45	334	34 9	115	5	HV33_MOUSE	IG HEAVY CHAIN V-III	1 266-47

ALIGNMENTS

RESULT 1
ID HV1A_HUMAN STANDARD: PRT; 117 AA.
AC P01742:
DT 21-JUL-1986 (REL. 01, CREATED)
DI 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-I REGION (EU).
OS HOMO SAPIENS (HUMAN).
CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; PRIMATES.
PN [1]
RP SEQUENCE.
RX MEDLINE: 71064024.
RA CUNNINGHAM R A, PITTSHAMSEP M, GALL W E, GOTTlieb P.D..
RA WAXDAL M.J., EDELMAN G.M.:
PL BIOCHEMISTRY 9:3161-3170(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE: 71064027.
RA GALL W E, EDELMAN G.M.:
PL BIOCHEMISTRY 9:3188-3196(1970).
CC -!- THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS MYELOMA PROTEIN HAS
CC ALSO BEEN DETERMINED.
DR PIR: A02023; GIHEU.
DF HSSP: P01810; LEVB.
KW IMMUNOGLOBULIN V REGION.
FT MOT_PES 1 1 PYRROLIDINE CARBOXYLIC ACID.
FT DISTILED 22 96
FT NONTER 117 117
SQ SEQUENCE 117 AA: 12477 MW: 10836175 DPC22:
Query Match 51.2%, Score 489, DB 5; Length 117;
Best Local Similarity 70.6%,
Pred. No. 1,226-81;
Matches 72; Conservative 16; Mismatches 9, Indels 5, Gaps 2.
CD 1 qvqlv-gsgaevskkqgsvskvskasggtfsisadilvridagqgylewmgdlyvnpfappo 59
QY 1 EVQLLESGAEVSKPKSSVKVSKASGDTISGVHITWVPAPQGLLEWMLDESIPFSSAN 60
Db 60 yaq----kfgrvritdestntaymelsrsdtafyca 97
QY 61 YAQYAAQKPEFFRVSTIATESISTSFIELSNLPDSTAYVYCA 102
RESULT 2
ID HV1B_HUMAN STANDARD: PRT; 117 AA.

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AC P01743;
DT 21-JUL-1986 (REL. 01, CREATED)
DI 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DI 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-I REGION (HG3)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES
RN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE: 83144028.
RA RECHAVI G., RAM D., GLAZER L., ZAKUT P., GIVOL D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 80:855-859(1983)
DR EMBL: J00240: G553411;
DR PIR: A02024: HVH035;
DR HSSP: P01810: IFVB;
KW IMMUNOGLOBULIN V REGION; SIGNAL;
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (HG3)
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 10028108 CPC12;

Query Match 46.58; Score 445; DB 5; Length 117;
Best Local Similarity 66.08; Pred. No. 7.54e-72;
Matches 68; Conservative 17; Mismatches 13; Indels 5; Gaps 4;

Db 20 qvqlv-qsgaevkkaevkssvkskasytfnysymhwrgapqqlwmg--i-inpsgg 75
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1 EVQLLEQSGAEVRFKPSVSVKSSVSKASGGTFSGHVITVWVQAPQGLEWMGESIPFGSAN 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 76 -stsyakfgqgrvmtldststvmelslrsdttavvyicar 117
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 YAQNYAQKFRDRVSIADSTSTSFIELSNLRSDDTAVVYICAR 103

RESULT 3
ID HV1G_HUMAN STANDARD; PRT: 117 AA.
AC P23083;
DT 01-NOV-1991 (REL. 20, CREATED)
DI 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DI 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-I REGION (V35)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES
RN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE: 86296408.
RA MATSUDA F., LEE K.H., NAKAI S., SATO T., KODAIRA M., ZONG S.Q.,
RL OHNO H., FUKUHARA S., HONJO T.;
RL EMBO J. 7:1047-1051(1988).
DR EMBL X07448: NOT_ANNOTATED_CDS
DR PIR: S00476: HVH035.
DR HSSP: P01810: IFVB;
KW IMMUNOGLOBULIN V REGION; SIGNAL;
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (V35)
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13009 MW; 10028108 CPC12;

Query Match 46.08; Score 440; DB 5; Length 117;
Best Local Similarity 66.08; Pred. No. 9.65e-71;
Matches 68; Conservative 13; Mismatches 17; Indels 5; Gaps 5;

Db 20 qvqlv-qsgaevkkaevkssvkskasytfnysymhwrgapqqlwmg-rinp-nsgg 76
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1 EVQLLEQSGAEVRFKPSVSVKSSVSKASGGTFSGHVITVWVQAPQGLEWMGESIPFGSAN 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 77 -t-syagkfgqgrvmtldststvmelslrsdttavvyicar 117
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 YAQNYAQKFRDRVSIADSTSTSFIELSNLRSDDTAVVYICAR 103

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RESULT 4
ID HV00_MOUSE STANDARD; PRT: 114 AA.
AC P01741;
DT 21-JUL-1986 (REL. 01, CREATED)
DI 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DI 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (ANTI-ANSONATP ANTIBODY);
OS MUS MUSCULUS (MOUSE)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA
RN [1]
PP SEQUENCE
RX STPAIN-A/J;
RX MEDLINE: 79195438.
RA CAPPA J.D., NIS-NOFF A.;
RL J. IMMUNOL. 123:279-284(1979);
DE -I- ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF THE IgG1
OC SUBCLASS. THERE WAS NO HELPER-GENEITY IN THE HEAVY CHAIN V REGION
KW IMMUNOGLOBULIN V REGION; ANTI-ANSONATP ANTIBODY;
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12555 MW; 1A027F1D CRC12;

Query Match 44.78; Score 427; DB 5; Length 114;
Best Local Similarity 63.38; Pred. No. 7.19e-68;
Matches 69; Conservative 22; Mismatches 12; Indels 6; Gaps 5;

Db 1 evql-qsgaevkkaevkssvkskasytfnysymhwrgapqqlwmg--sssa 56
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1 EVQLLEQSGAEVRFKPSVSVKSSVSKASGGTFSGHVITVWVQAPQGLEWMGESIPFGSAN 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 57 yp-nyagkfgqgrvmtldststvmelslrsdttavvyicarvisry 104
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 YAQNYAQKFRDRVSIADSTSTSFIELSNLRSDDTAVVYICAR 104

RESULT 5
ID HV1G_HUMAN STANDARD; PRT: 143 AA.
AC P01744;
DT 21-JUL-1986 (REL. 01, CREATED)
DI 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DI 01-NOV-1991 (REL. 15, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-I REGION (ND) (FRAGMENTS);
OS HOMO SAPIENS (HUMAN);
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES
RN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE: 83065234.
RA KENTEN J.H., MARGAARDE H.V., ROBERTSON M., DEPRYSHIRE P.P., VINEY J.;
RL BELL D.O., GOULD H.J.;
PL PROC. NATL. ACAD. SCI. U.S.A. 79:6661-6665(1982);
RN [2]
PP SEQUENCE OF 16-142.
RA BENNICH H.H., JOHANSSON S.G.O., VON BAHN-LINDSTROM H.;
RL (IN) IMMEDIATE HYPERSENSITIVITY: MODERN CONCEPTS AND DEVELOPMENTS.
P: RACH M.K., ED., PT. 1:36, MASCHE DEKKEP, NEW YORK, (1978).
CC -I- THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A02026: EIHUND.
DR HSSP: P01607: IFGV;
KW IMMUNOGLOBULIN V REGION; SIGNAL;
FT NON_TER 4 5
FT SIGNAL 1 15
FT CHAIN 16 143 IG HEAVY CHAIN V REGION (ND)
FT MCD_RES 16 16 PEROXIDASE-CARBOXYLIC ACID
FT DISULFID 37 111
FT CONFLICT 17 17
FT CONFLICT 49 50
FT CONFLICT 62 64
FT CONFLICT 121 121
FT NON_TER 143 143

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SQ SEQUENCE 143 AA: 16051 MW: 50605EL3 CPG32;
 Query Match 44.4%, Score 424, DR 5, Length 143
 Best Local Similarity 52.6%, Pred. No. 3, 30e-67;
 Matches 70, Conservative 24, Mismatches 23, Indels 6, Gaps 6;
 Db 15 qqlv-gsgaevkpgssvskksggtyftsyglnwvkprgqglewlg-yinp-gng-y 72
 QY 1 EVOLLEQSGAEVPRKPGSSVKVSKKSGGTFSGHVTWVPAQPGGLEWMSGESIPFGSAN 60
 Db 73 t-nvaprfggvtmrdsafstaymdlrslrdsdsvfycakspdfswdyndysytl 130
 QY 61 YACNYAKKFPDPVPSIADSTSTFIELSNLSDTAVVYCAPGPPYCSA-SGVPYDFE 119
 Db 131 dwgggtttvss 143
 QY 120 QWGGGTLTVSS 132
 RESULT 6
 ID HV02-MOUSE STANDARD: PPT: 140 AA
 AC P01746;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (93G7).
 OS MUS MUSCULUS (MOUSE).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 PC STRAIN-A/J;
 PX MEDINF: P0152918.
 RA SIMS J., BARRITTIS T.H. ESTESS P., SLAUGHTER C., TUCKER P.W.,
 RA CAPRA J.D., 309-311(1982).
 RL SCIENCE 216-309-311(1982).
 DP EMRL: J00493; G195007;
 DP PIP: A02028; HVMG7
 DP HSSP: P01789; 6FAR
 KW IMMUNOGLOBULIN V REGION: ANTIAPSONATE ANTIBODY; HYPERIDOMA; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION (93G7).
 FT NON-TER 140 140
 SQ SEQUENCE 140 AA: 15514 MW: 0700DSC8 CPG32;
 Query Match 43.5%, Score 416, DR 5, Length 140;
 Best Local Similarity 51.5%, Pred. No. 1, 90e-65;
 Matches 68, Conservative 30, Mismatches 23, Indels 11, Gaps 10;
 Db 20 evl-gsgaevkpgssvskksggtyftsyglnwvkprgqglewlg-yinp-gng-y 75
 QY 1 EVOLLEQSGAEVPRKPGSSVKVSKKSGGTFSGHVTWVPAQPGGLEWMSGESIPFGSAN 60
 Db 76 yinp-gsgaevkpgssvskksggtyftsyglnwvkprgqglewlg-yinp-gng-y 129
 QY 61 YACNYAKKFPDPVPSIADSTSTFIELSNLSDTAVVYCAPGPPYCSA-SGVPYDFE 129
 Db 129 ywgggtttvss 140
 QY 121 QWGGGTLTVSS 132
 RESULT 7
 ID HV02-MOUSE STANDARD: PPT: 120 AA
 AC P01747;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (36-65).
 OS MUS MUSCULUS (MOUSE).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PODENTIA.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE: 83131846.
 PA STEKEVITZ M., GEFTER M.L., PRODEUR P., FIEBELT R.,
 PA MAPSHAKI-ROTHSTEIN A.;
 PL EUP J. IMMUNOL 12-1023-1022(1992).
 CC -1- FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES
 CC THAT HYPERIDOME TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF
 CC THESE V REGIONS HAVE REARRANGED TO THE SAME J SEGMENT, JH2.
 DR PIR: A03028; HVMG7.
 DR HSSP: P01789; 6FAR.
 KW IMMUNOGLOBULIN V REGION: ANTIAPSONATE ANTIBODY; HYPERIDOMA.
 FT NON-TER 120 120
 SQ SEQUENCE 120 AA: 33307 MW: BRAR0CA1 CPG32;
 Query Match 43.1%, Score 412, DR 5, Length 120;
 Best Local Similarity 50.4%, Pred. No. 1, 44e-64;
 Matches 66, Conservative 32, Mismatches 23, Indels 11, Gaps 10;
 Db 1 vql-gsgaevkpgssvskksggtyftsyglnwvkprgqglewlg-yinp-gng-y 56
 QY 2 VOLLEQSGAEVPRKPGSSVKVSKKSGGTFSGHVTWVPAQPGGLEWMSGESIPFGSAN 61
 Db 57 t-ympokfkgtlttdkssstaymdlrslrdsdsvfycakspdfswdyndysytl 109
 QY 62 AANYAKKFPDPVPSIADSTSTFIELSNLSDTAVVYCAPGPPYCSA-SGVPYDFE 121
 Db 110 wgggtttvss 120
 QY 122 QWGGGTLTVSS 132
 RESULT 8
 ID HV16-HUMAN STANDARD: PPT: 124 AA.
 AC P01761;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V-I REGION (SIE).
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 82046599.
 RA ANDREWS D.W., CAPRA J.D.;
 RA BIOCHEMISTRY 20:5822-5830(1981).
 CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
 CC ACTIVITY.
 DR PIR: A02044; MHUS1.
 DR HSSP: P01857; 2FGW.
 KW IMMUNOGLOBULIN V REGION.
 FT NON-TER 124 124
 SQ SEQUENCE 124 AA: 13732 MW: CLE9663D CPG32;
 Query Match 42.5%, Score 406, DR 5, Length 124;
 Best Local Similarity 50.8%, Pred. No. 1, 90e-63;
 Matches 67, Conservative 27, Mismatches 28, Indels 10, Gaps 8;
 Db 1 qqlv-gsgaevkpgssvskksggtyftsyglnwvkprgqglewlg-yinp-gng-y 57
 QY 1 EVOLLEQSGAEVPRKPGSSVKVSKKSGGTFSGHVTWVPAQPGGLEWMSGESIPFGSAN 60
 Db 58 fggvyl-k-wrvvtskpsfndaymdlrslrdsdsvfycakspdfswdyndysytl 110
 QY 61 YACNYAKKFPDPVPSIADSTSTFIELSNLSDTAVVYCAPGPPYCSA-SGVPYDFE 120
 Db 111 ywgggtttvss 122
 QY 121 QWGGGTLTVSS 132
 RESULT 9

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FT      HELIX      29      31
FT STRAND      34      39
FT TURN      41      42
FT STRAND      46      51
FT TURN      53      54
FT STRAND      58      60
FT TURN      62      67
FT STRAND      68      73
FT TURN      74      77
FT STRAND      78      83
FT HELIX      88      90
FT STRAND      92      99
FT STRAND      106     106
FT TURN      107     108
FT STRAND      109     109
FT STRAND      113     113
FT STRAND      120     124
FT STRAND      120     124
SQ SEQUENCE      126 AA; 13718 MW; 14F328CF CRC32;

Query Match      42.48; Score 405; DR 5; Length 126;
Best Local Similarity 45.94; Pred. No. 4,97e-63;
Matches      61; Conservative      33; Mismatches      31; Indels      8; Gaps

Db      1 qvqlve-sgggvqvqgrslrlscsssgflfssyanywvirqpqakleww--al-ixddus 56
      qvqlve-sgggvqvqgrslrlscsssgflfssyanywvirqpqakleww--al-ixddus 56
      1 EVLLLEIS5AEVKKPKSSSVKVS--KASGGTF--SCHVITWVPOAPGQGLFMMGESLPIHESAN 60
      EVLLLEIS5AEVKKPKSSSVKVS--KASGGTF--SCHVITWVPOAPGQGLFMMGESLPIHESAN 60

Db      57 -dqhyadvskgrflsrldskntllflqmsdlrpedtqvvyfcardqqlatfssasctapdy 115
      -dqhyadvskgrflsrldskntllflqmsdlrpedtqvvyfcardqqlatfssasctapdy 115
      61 YAQNTYACKERFRVSTACESTSTSFIELSNLESTGTAIVYQARPPK-YGSAGKRYVDF 119
      YAQNTYACKERFRVSTACESTSTSFIELSNLESTGTAIVYQARPPK-YGSAGKRYVDF 119

Db      116 --wgggtpvtvss 126
      --wgggtpvtvss 126
      120 GQWGS5TLIVTSS 132
      GQWGS5TLIVTSS 132

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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DI DT 13-AUG-1987 (REL. 05, LAST ANNOTATION UPDATE)
DT DT 13-AUG-1987 (REL. 05, LAST ANNOTATION UPDATE)
DI DT IG HEAVY CHAIN V REGION (MPC 11).
DI DT Q5 MUS MUSCULUS (MOUSE).
DI DT QS EUKARYOTA; METAZOA;
DI DT OC EUROTHERIA; RODENTIA.
DI DT [1]
DI DT RP SEQUENCE FROM N.A.
DI DT RX MEDLINE: 81053741.
DI DT RL ZAKUT F., COHEN J., GIVOL D.;
DI DT RL NUCLEIC ACIDS RES. 8:3591-3601(1980).
DI DT [2]
DI DT RP REVISIONS.
DI DT RP ZAKUT R., COHEN J., GIVOL D.;
DI DT RL NUCLEIC ACIDS RES. 8:4839-4840(1980).
DI DT CC -:- THIS SEQUENCE WAS TRANSLATED FROM AN MPNA ISOLATED FROM A
DI DT CC MELOMA IHAL SECRETES 1GGZF.
DI DT RP PIP: AG2027; GVMS11.
DI DT DR HSP; PO1810; IMF.
DI DT KW IMMUNOGLOBULIN V REGION.
DI DT FT NON_TER 121 121
DI DT SEQUENCE 121 AA; 13135 MW; 2AEF80CC CRC32;

Query March 41.2% Score 334, ID 5, Length 121;
Best Local Similarity 46.2%, Pred. NO. 1,27e-60;
Matches 51; Conservative 36; Mismatches 22; Indels 11; Gaps

Db 1 eaql-qsgaelvrptskvkskaagvtfnynjdwkcrphdhwld--vlypqad 56
Qy ||| ||||| ||| ||||| ||||| ||| ||||| ||||| ||| |||
Qy 1 FVGIIFSGAFVKKPKSSVKVSKKAGRTFSGHVTIWRGAPKPTWMMFSTPRSAN 60
Db 57 ft-nyndnkgkailkadssataviqissitdsdaalyhcarr--vlyps--p-yld 109
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Release 2.1D John F. Collins, PicoComputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Pin on: Tue Feb 24 07:05:52 1998; MasPar time 6.99 Seconds
252.448 Million cell updates/sec

Tabular output not generated.

Title: >US-08-844-215-2
Description: (1:127) from US08844215.paf
Perfect Score: 931

Sequence: 1 EVQLLEQSGAEVKRPGSSVK.....HTMGYFDYWGQGLTVVSS 127

Scoring table: PAM 150
Gap 11

Searched: 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq30
1:part1 2:part3 3:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 30.758; Variance 161.149; scale 0.191

Pred. NO is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	616	66.2	147	12	93KA9 anti-Varicella	1.27e-38
2	613	55.8	123	23	CEA-specific antibody	2.20e-38
3	610	55.8	481	5	Sequence of antibody	3.81e-38
4	602	64.7	123	23	CEA-specific antibody	1.65e-37
5	601	64.7	123	23	CEA-specific antibody	1.98e-37
6	600	64.4	123	23	CEA-specific antibody	2.37e-37
7	597	64.1	123	23	CEA-specific antibody	4.10e-37
8	579	62.2	120	9	SPA-reactive IgM heavy	1.10e-35
9	576	61.9	476	6	Antibody D heavy chain	1.90e-35
10	574	61.7	120	9	SPA-reactive IgM heavy	2.74e-35
11	572	61.4	98	12	DPLC VH region	3.94e-35
12	572	61.4	249	14	Humanised 5G1.1 VH +	3.94e-35
13	565	60.7	124	14	HSV-neutralising anti	1.41e-34
14	561	60.4	249	14	Humanised 5G1.1 VH +	2.93e-34
15	558	59.9	119	23	Anti-melanoma antibod	5.06e-34
16	558	59.5	140	23	Humanised heavy chain	5.06e-34
17	554	59.5	248	14	Humanised CDR-grafted	1.05e-33
18	550	59.1	98	12	Humanised VH region	2.17e-33
19	550	59.1	117	4	Human heavy chain V r	2.17e-33
20	550	59.1	117	4	Protein encoded by th	2.17e-33

21	550	59.1	117	20	W03950	DNA fragment vha9.8;	2.17e-33
22	549	59.0	140	23	W21849	Humanised heavy chain	2.61e-33
23	548	58.9	121	14	R77974	Humanised mouse DPO-2	3.13e-33
24	548	58.9	124	9	R45604	Monoclonal antibody G	3.13e-33
25	548	58.9	140	9	R55556	DPO-200 Humanised an	3.13e-33
26	546	58.6	121	16	R88504	VHmu for antibody B13	4.50e-33
27	546	58.6	142	9	R50188	Heavy chain variable	4.50e-33
28	543	58.3	117	2	R41104	Human antibody Ea hea	7.78e-33
29	543	58.3	118	5	R28742	Heavy chain variable	7.78e-33
30	540	58.0	121	5	R25734	Humanised VH region o	1.34e-32
31	540	58.0	140	23	W21850	Humanised heavy chain	1.34e-32
32	535	57.5	142	9	R50194	Heavy chain variable	2.33e-32
33	535	57.5	248	14	R77607	Humanised CDR-grafted	3.33e-32
34	535	57.5	249	14	R77611	Humanised 5G1.1 VH +	3.33e-32
35	535	57.5	468	5	R24804	pre-5A8 humanised hea	3.33e-32
36	531	57.0	124	8	R47931	Mutated humanised hea	5.90e-32
37	531	57.0	140	12	R64265	CDR-grafted L243-qH V	5.90e-32
38	521	57.0	140	12	R64265	Humanized anti-body I2	6.90e-32
39	520	56.9	139	11	R62679	CY1748PHB VH region	8.27e-32
40	526	56.5	124	9	R45610	Monoclonal antibody G	1.71e-31
41	526	56.5	139	12	R62578	CY1748PHB VH region	1.71e-31
42	526	56.5	139	8	R43693	PB1.3/Humanised heavy	1.71e-31
43	526	56.5	139	11	R62680	CY1748PHC VH region	1.71e-31
44	526	56.5	139	8	R43689	PB1.3/Humanised heavy	1.71e-31
45	525	56.4	118	4	R22569	Heavy chain VH15.4 fr	2.05e-31

ALIGNMENTS

RESULT	1
ID	R65019 standard; Protein; 147 AA.
AC	R65019;
DI	02-OCR-1995 (first entry)
DE	93KA9 anti-Varicella zoster virus antibody heavy chain variable.
DE	region.
KW	Varicella zoster virus; VZW; anti-VZW monoclonal antibody; 93KA9;
OS	glycoprotein II subunit; vaccine.
EH	Synthetic.
FT	Protein
FT	Key
FT	Location/Qualifiers
FT	20..147
FT	mature light chain
FT	Region
FT	50..54
FT	/label= complementarity determining region (CDR)
FT	Region
FT	69..85
FT	/label= CDR
FT	Region
FT	118..136
FT	/label= CDR
FN	W09504080-A.
PD	09-FEB-1995.
PF	22-JUL-1994; U08241.
PR	28-JUL-1993; US-098479.
PR	24-MAR-1994; US-217918.
PA	(SANO) SANDOZ PHARM CORP
PI	Lake Pl, Ostberg L;
DR	WPI; 95-090612/12.
DP	N-PSDB; 082750.
FT	Human monoclonal antibodies specific for the glycoprotein II
FT	subunit of varicella zoster virus - used in a therapy and
FT	prophylaxis of infection
PS	Claim 8; Fig 4B; 39pp; English.
CC	A human anti-varicella zoster virus monoclonal antibody was prep
CC	One using the tritoma method of Ostberg et al. (1983) Hybridoma 2:351-367.
CC	This cell line designated cell line TC93KA9 produced an antibody
CC	designated 93KA9. cDNA for the light and heavy chain variable region
CC	genes of the 93KA9 antibody were cloned using PCR. At least two
CC	heavy chain (gamma-1) and two light chain (kappa) specific clones
CC	were sequenced (see G62749 & G83750 respectively).
SQ	Sequence 147 AA:

Query Match 66.2%; Score 115; DB 12; Length 147;
Best Local Similarity 66.7%; Prod No. 1.27e-38;
Matches 86; Conservative 19; Mismatches 22; Indels 2; Gaps 0;

Db	60	yackfagrltitadeststajmolsclrsedlatvyyvcarhcheycl-yy-ymydwagqa	115
QY	61	YACKFQGSLEIACDSTAIYMEISSLPSSETAVYFCAPVVPKAIPTHTMYFFIHWEG	120
Db	117	tmvtvss 123	
QY	121	tmvtvss 127	

RESULT	3
ID	P24442 standard; Protein; 481 AA.
AC	P24442.
DI	Q2-JAN-1992 (first entry)
DE	Sequence of antibody molecule IgG1.
KW	Antibody; immunoglobulin G1.
OS	Home sapiens.
FH	Key
	Location/Qualifiers

[illegible]

Db 144 gtlvtvss 151
 QY 120 gtlvtvss 127

RESULT 4
 ID W19886 standard. Protein. 123 AA.
 AC W19886;
 DT 07-DEC-1997 (first entry)
 DE CEA-specific antibody CEA6 VH mutant TO6D10 sequence.
 KW Carcinoembryonic antigen; CEA; human; antibody; scFv;
 KW tumour marker; lung cancer; breast cancer; colon cancer;
 KW adenocarcinoma; diagnosis.
 OS Chimeric Homo sapiens;
 FH Key Location/Qualifiers
 FT Region 31...35
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 50...66
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 99...112
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 PN W09720932-A1.
 PD 12-JUN-1997.
 PF 09-DEC-1996; G03043.
 PF 11-OCT-1996; GB-021295.
 PR 07-DEC-1995; GB-025004.
 PR 23-MAY-1996; GB-010824.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Allen DJ, McCafferty JG, Osbourn JK;
 DF WPI: 97-119779/29.

Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing cancer
 PS Claim 4: Fig 2, 128pp; English.
 CC This polypeptide sequence comprises the heavy chain variable region (VH), HBB6, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see W19881). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1×10^{-8} M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W19876-85), or their CDR sequences, as well as CEA6 VH and VL variants (see W19886-95) obtained by mutagenesis or chain shuffling. An example of a claimed pairing is HBB6 VH with CEA6 VL (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast.
 SQ Sequence 123 AA;

Query Match 64.7%; Score 602; DB 23; Length 123;
 Best Local Similarity 71.7%; Pred. No. 1.65e-37;
 Matches 91; Conservative 10; Mismatches 22; Indels 4; Gaps 3;
 Db 1 qvqlv-qsgaevkpkssvkscasggtfnsplnwlrqapqqlwmgslipstgtan 59
 QY 1 EVALLQSGAEVKKPSSVKVSCQVFDTSRYTTQWLPCAPQGPENMGIIPYNTPN 60
 60 yadkfgrlritadeststymelsrlrsdtaavyagrshtyel-yy--yymdvwwggg 116
 QY 61 YAQKFGRLSITADDTSTAYMFLSLRSEDIAVYFCAPVTPNAPHTMGYFYFWGQ 120
 Db 117 tmvtvss 123
 QY 121 TLTVSS 127

RESULT 6
 ID W19881 standard. Protein. 123 AA.
 AC W19881;
 DT 07-DEC-1997 (first entry)

RESULT 5
 ID W19886 standard. Protein. 123 AA.
 AC W19886;
 DT 07-DEC-1997 (first entry)
 DE CEA-specific antibody CEA6 VH mutant TO6D10 sequence.
 KW Carcinoembryonic antigen; CEA; human; antibody; scFv;
 KW tumour marker; lung cancer; breast cancer; colon cancer;
 KW adenocarcinoma; diagnosis.
 OS Chimeric Homo sapiens;
 FH Key Location/Qualifiers
 FT Region 31...35
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 50...66
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 99...112
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 PN W09720932-A1.
 PD 12-JUN-1997.
 PF 09-DEC-1996; G03043.
 PF 11-OCT-1996; GB-021295.
 PR 07-DEC-1995; GB-025004.
 PR 23-MAY-1996; GB-010824.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Allen DJ, McCafferty JG, Osbourn JK;
 DF WPI: 97-119779/29.
 Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing cancer
 PS Claim 4: Fig 2, 128pp; English.
 CC This polypeptide sequence comprises the heavy chain variable region (VH), TO6D10, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see W19881). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1×10^{-8} M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W19876-85), or their CDR sequences, as well as CEA6 VH and VL variants (see W19886-95) obtained by mutagenesis or chain shuffling. Examples of claimed pairings are TO6D10 VH with TO6D12 or CEA6 VL. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast.
 SQ Sequence 123 AA;

Query Match 64.5%; Score 601; DB 23; Length 123;
 Best Local Similarity 71.7%; Pred. No. 1.98e-37;
 Matches 91; Conservative 10; Mismatches 22; Indels 4; Gaps 3;
 Db 1 qvqlv-qsgaevkpkssvkscasggtfnsplnwlrqapqqlwmgslipstgtan 59
 QY 1 EVALLQSGAEVKKPSSVKVSCQVFDTSRYTTQWLPCAPQGPENMGIIPYNTPN 60
 60 yadkfgrlritadeststymelsrlrsdtaavyagrshtyel-yy--yymdvwwggg 116
 QY 61 YAQKFGRLSITADDTSTAYMFLSLRSEDIAVYFCAPVTPNAPHTMGYFYFWGQ 120
 Db 117 tmvtvss 123
 QY 121 TLTVSS 127

	OS	Chimeric Homo sapiens:
	FH	Chimeric synthetic.
	Key	Location/Qualifiers
	Region	31..35
	/Label=	CDR1
	/note=	"complementarity determining region 1"
	Region	50..66
	/Label=	CDR2
	/note=	"complementarity determining region 2"
	Region	99..112
	/Label=	CDR3
	/note=	"complementarity determining region 3"
	FT	WC-9720932-A1.
	PB	12-JUN-1997.
	PD	09-DEC-1996; G03043.
	PF	11-OCT-1996; GR-021295.
	PR	07-DEC-1995; GR-025004.
	PT	23-MAY-1996; GR-01824.
	PA	(CAMP)- CAMPIDGE ANTIBODY TECHNOLOGY.
	PI	Ailen D J McCafferty JG, Osbourn JK;
	DI	WPl: 97-319779/29.
	PT	Specific binding markers for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing cancer
	PS	Claim 4; Fig 2; 128pp; English.
	CC	This polypeptide sequence comprises the heavy chain variable region (VH), HBA1L, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see W19881). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1×10^{-8} M, is non-cross reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W19876-85), or their CDR sequences, as well as CEA6 VH and VL variants (see W19884-94) obtained by mutagenesis or chain shuffling. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g adenocarcinoma of the colon, lung or breast.
	SQ	Sequence 123 AA;
		Query Match 64 % Score 507; Pos 23; Length 123;
		Best Local Similarity 71 %; Prod No 4 10e-37;
	Matches	91; Conservative 14; Mismatches 18; Indels 4; Gaps
Dd	1	gqqlv-qsgaevkkgsskvkscaagqtispslwlraqpqglwmassilprstqm 59
EY	1	EYLLEFGSGAEKVFSSVPVS-QVEGLIFSHYIIGELFAPNCFMSESLFAVRTR 60
Dd	60	yakfqurlitadestaymclsksdslavyyea-a-dnsenrSYTYmdrrqq 116
EY	61	VAKRFEGEQLSITAGSTAYWEISLSLFETAVYFAPVVIPNAIEFTWCVYEWQQ 120
Lb	117	lmvlvss 123
Qy	121	tlvtvss 127
RESULT 8		
ID	R54796 standard; peptide; 120 AA.	
AC	R54796;	
DT	18-OCT-1994 (first entry)	
DE	SpA-reactive IgM heavy chain clone KAS.	
KW	SpA domain D; Ig binding region; Igm; B-cell supernatant; SAM;	
KX	superantigen; heavy chain variable region; VH3 restricted antibody;	
KS	VE, protein-A, KAS, B lymphocyte, vaccine,	
KW	Homo sapiens.	
PN	WO9409818-A.	
PP	11-MAY-1994.	
PF	29-OCT-1993; U10555.	
PP	30-OCT-1992; US-660416.	
PA	(REGC) UNIV CALIFORNIA.	

PI Silverman GJ;
 DR WPI: 94-167127/20.
 PT Stimulating prodn. of variable region gene family restricted
 PT Antibodies - through B-cell super-antigen vaccination
 PS Disclosure; Page 78; 130pp; English.
 CC A B-cell superantigen (sAg) is a fragment of SpA D domain that
 CC specifically binds the Fab portion of variable region of VH, especially
 CC antibodies. The sAg is used to enhance production of VH, especially
 CC VH3, restricted Abs. During attempts to identify sAgs, aa sequences
 CC (R54784-801) of H chains from Ig reactive with mod-SpA, and aa and
 CC DNA sequences (P54802-16, Q44842-56) of VH regions of SpA binders
 CC obtained from combinatorial libraries were determined. IgM protein
 CC KAS is derived from the germline configuration of a VH gene
 CC segment.
 SQ Sequence 120 AA;
 Query Match 62.2%; Score 579; DB 9; Length 120;
 Best Local Similarity 67.5%; Pred. No. 1.10e-35;
 Matches 85; Conservative 17; Mismatches 18; Indels 6; Gaps 3;
 Db 1 vhlv-qsgaevkpkssvkvscasgggtfssvsaivswvraqpgglwmggiipfgqany 59
 QY 2 VQLLESGAEVKKFGSVKSVKSCQVFGDTSFRYIIQLWLPQAPQGPPEWNGNIIVNTFNY 61
 Db 60 aqkgirvritadesntaymelrslrsddtamvycakegydygr-p-----fdfwgggt 114
 QY 52 AKKQKELSLFALTSLSIAVMELSLSPSTAVYFCAPVW:FNALPHVWGYVFEWVGJST 121
 Db 115 lvtvss 120
 QY 122 LVTVSS 127
 RESULT 9
 ID F31022 standard; Protein; 476 AA.
 AC R31023;
 DT 19-MAY-1993 (first entry)
 DE Antibody D heavy chain.
 KW Heavy, light, chain; antibody; D; monoclonal; peripheral; blood;
 KW lymphocyte; hepatitis A virus; HAV; sero; positive; patient;
 KW murine; B583; polyadenylated; cDNA library; human; kappa; L; H.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "Signal peptide"
 FT /Region 20..49
 FT /label= FR1
 FT /Region 50..54
 FT /label= CDR1
 FT /Region 55..68
 FT /label= FR2
 FT /Region 69..84
 FT /label= CDR2
 FT /Region 85..113
 FT /label= FR3
 FT /Region 114..121
 FT /label= CDR3
 FT /Region 122..132
 FT /label= FR4
 FT /Domain 133..241
 FT /label= CH1
 FT /Region 242..262
 FT /label= HINGE
 FT /Domain 263..379
 FT /label= CH2
 FT /Domain 380..497
 FT /label= CH3
 FN EP-523949-A.
 PD 20-JAN-1993.
 PF 14-JUL-1992; 306420.
 PR 15-JUL-1991; GB-015284.
 PR 01-AUG-1991; GB-016594.
 PR 23-MAY-1992; GB-006294.

PA (WELL) WELLCOME FOUND LTD.
 PI Crowe JS, Lewis AP;
 DR WPI: 93-019951/03.
 DR N-PSDB: Q35099.
 PT Prodn. of recombinant primate antibodies - useful for treating
 PT infections caused by hepatitis A, B and C, herpes,
 PT cytomegalovirus, AIDS, APC, also treat multiple sclerosis,
 PT arthritis etc.
 PS Disclosure; Fig 2: 35pp; English.
 CC The sequences given in R31023-24 represent the heavy and light chains
 CC of Antibody D respectively. Antibody D is a monoclonal antibody which
 CC was derived from peripheral blood lymphocytes from a hepatitis A virus
 CC (HAV) sero positive patient. Antibody D is closely related in nature
 CC to murine antibody B5B3. Total RNA was isolated from antibody D
 CC expressing cells and polyadenylated RNA was extracted. These polyA
 CC RNA's were used to prepare a cDNA library which was screened for human
 CC kappa light (L) chains and two positive clones were detected.
 CC Further heavy (H) chain clones were also isolated.
 SQ Sequence 476 AA;
 Query Match 61.9%; Score 576; DB 6; Length 476;
 Best Local Similarity 67.4%; Pred. No. 1.90e-35;
 Matches 87; Conservative 15; Mismatches 22; Indels 4; Gaps 3;
 Db 20 qmgv-qsgaevkpkssvkvscasgggtfssvsaivswvraqpgglwmggiipfgtpt 78
 QY 1 EVVLLESGAEVKKFGSVKSVKSCQVFGDTSFRYIIQLWLPQAPQGPPEWNGNIIVNTFN 50
 Db 79 ysqnfgvritadeststahmelrslrsddtamvycatdryqanfdrrvqg-fdppq 137
 QY 61 YAKQKQRLSITADSTSTAYMELSLSPEDTAVYFCA--PVVIPNAPHTWGYVFDYWG 118
 Db 138 qgtlvvss 146
 QY 119 QGILVIVSS 127
 RESULT 10
 ID R54795 standard; peptide; 120 AA.
 AC R54795;
 DT 18-OCT-1994 (first entry)
 DE SPA-reactive IgM heavy chain clone BOR.
 KW SPA domain D; Ig binding region; IgM; B-cell superantigen; sAg;
 KW superantigen; heavy chain variable region; VH3 restricted antibody;
 KW VH; protein-A; BOR; B-lymphocyte; vaccine.
 OS Homo sapiens.
 PN WC9409818-A.
 PD 11-MAY-1994.
 PF 29-OCT-1993; U10555.
 PF 30-OCT-1992; US-969936.
 PA (PEGC) UNIV CALIFORNIA.
 PI Silverman GJ;
 DR WPI: 94-167127/20.
 PT Stimulating prodn. of variable region gene family restricted
 PT antibodies - through B-cell super-antigen vaccination
 PS Disclosure; Page 77; 130pp; English.
 CC A B-cell superantigen (sAg) is a fragment of SpA D domain that
 CC specifically binds the Fab portion of variable region of VH, especially
 CC antibodies. The sAg is used to enhance production of VH, especially
 CC VH3, restricted Abs. During attempts to identify sAgs, aa sequences
 CC (R54784-801) of H chains from Ig reactive with mod-SpA, and aa and
 CC DNA sequences (R54802-16, Q44842-56) of VH regions of SpA binders
 CC obtained from combinatorial libraries were determined. IgM protein
 CC BOR is derived from the germline configuration of a VH gene
 CC segment.
 SQ Sequence 120 AA;
 Query Match 61.7%; Score 574; DB 9; Length 120;
 Best Local Similarity 69.8%; Pred. No. 2.74e-35;
 Matches 88; Conservative 15; Mismatches 17; Indels 6; Gaps 3;
 Db 1 vqlv-qsgaevkpkssvkvscasgggtfssvsaivswvraqpgglwmggiipfgtpt 59
 QY 2 VQLLESGAEVKKFGSVKSVKSCQVFGDTSFRYIIQLWLPQAPQGPPEWNGNIIVNTFNY 61

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QY 2 VALLPSSAEKVKPKSSVKVSKVQVGRVTFPSVYTIQWVQAPAGGCPGPMWGNIIIPVYNTPNV 61
Db 60 aqlfagartttdestatymessirsdatalyycaesrrmai n f gfwgqgt 114
   ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 AQKFGRLSITADSTSTAYMELSSKSDTAVYFCARVVPNAIRHTMGYYEDYWGQGT 121
Db 115 lvtvss 120
   |||||
QY 122 LVTVSS 127
   |||||

RESULT 11
ID R72068 standard; Protein: 98 AA.
AC R72068:
DE 26-SEP-1995 (first entry)
DE DP10 VH region.
KW Graves ophthalmopathy associated immunoglobulin protein;
KW orbital antigen, monoclonal antibody; heavy chain, H chain,
KW variable region; autoimmunity.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDP1
FT Region 50..66
FT /label= CDR2
FT /label= CDR2
PN W09508336-A.
PD 30-MAR-1995.
PF 22-SEP-1994; U10756.
PR 22-SEP-1993; US-124469.
PA (NICH-) NICHOLS INST DIAGNOSTICS.
PI McLachlan SM, Rapoport B;
DR WPI: 95-139383/18.
DR N-PSDB: Q89327.
PT Graves' ophthalmopathy-associated monoclonal antibody - produced
PT by molecular cloning of immunoglobulin genes by PCR
PS Disclosure: Page 68; 94pp; English.
CC L- and H-chain DNA was amplified by PCR from Graves' orbital
CC tissue and clones encoding autoimmune-associated immunoglobulin
CC fragments were obtained. 13/15 clones of H chain (IgG1) genes
CC showed homology to the closest germline genes, DP10 (Q89327) and
CC h1263 (Q89328). The DNA (Q89329) and corresp. amino acid
CC (R72070) sequences of the VH region of a representative clone,
CC OF7H1.2, are provided.
SQ Sequence 98 AA;

Query Match 61.4%; Score 572; DB 12; Length 98;
Best Local Similarity 78.8%; Pred. No. 3,94e-35;
Matches 78; Conservative 11; Mismatches 9; Indels 1; Gaps 1;

Db 1 qvqlv-qsgaevkpkgsavkvsckasgtfssvaiswvrgapqgglewmgliipfgtan 59
   |||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLEQSGAEVKPKSSVKVSKVQVGRVTFPSVYTIQWLRQAPGSGPMMGNIIIPVYNTPN 60
Db 60 yaqkfqrvtadeststaymelssirsdetavyyicar 98
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YAKFKGRLSITADSTSTAYMELSSURSEDAVYFCAR 44
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
ID R77610 standard; Protein: 249 AA
AC R77610:
DE 15-MAR-1996 (first entry)
DE Humanised 5G1.1 VH + IGHRL.
KW Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= sig_peptide
FT Peptide 20..249
FT /label= mat_peptide
FT Region 45...54

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FT /label= CDR-H1 69...79
FT Region CDR-H2
FT /label 118 130
FT Region CDR-H3
PN W09529697-A1.
PD 09-NOV-1995.
PF 01-MAY-1995; W05688.
PR 02-MAY-1994; US-236208.
PA (ALEX-) ALEXION PHARM INC.
PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins SJ,
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
DP WPI: 95-392923/50
DR N-PSDB: T08483.
PT Treating glomerulonephritis with antibody against complement C5
PI Component - to inhibit complement induced cell lysis
FS Example 11, Page 119-122, 181pp, English.
CC A humanised CDK-grafted and framework sequence-altered Fd, 5G1.1 VH
CC + IGHRL (P77610). Includes CDRs derived from mouse anti-C5 monoclonal
CC antibody 5G1.1. It can be co-expressed with a humanised light
CC chain (P77612) in human 2A+ RNA cells using encoding DNAs
CC subcloned into vector APEX-3P (T08476). Such humanised recombinant
CC antibodies retain the ability of mAb 5G1.1 to block human complement
CC C5a generation and thus to reduce glomerular inflammation and kidney
CC dysfunction associated with glomerulonephritis.
SQ Sequence 249 AA;

Query Match 61.4%; Score 572; DB 14; Length 249;
Best Local Similarity 68.5%; Pred. No. 3.94e-35;
Matches 87; Conservative 16; Mismatches 19; Indels 5; Gaps 3;

Db 20 qvqlv-qsgaevkpkgsavkvsckasgtfssvaiswvrgapqgglewmgliipfgtan 78
   |||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLEQSGAEVKPKSSVKVSKVQVGRVTFPSVYTIQWLRQAPGSGPMMGNIIIPVYNTPN 60
Db 79 yaqkfqrvtadeststaymelssirsdetavyyicar 144
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 YAKFKGRLSITADSTSTAYMELSSURSEDAVYFCAR 44
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 135 lvtvss 141
   |||||
QY 121 LVTVSS 127
   |||||

RESULT 13
ID R76964 standard; peptide: 122 AA.
AC R76964:
DE 22-FEB-1996 (first entry)
DE HSV-neutralising antibody clone FabHSV8 heavy chain.
KW Herpes simplex virus, type 1, type 11, monoclonal antibody;
KW diagnosis; neutralisation; immunotherapy.
OS Homo sapiens.
PN W09518634-A1.
PD 13-JUL-1995.
PF 04-JAN-1995; U06067.
PR 04-JAN-1994; US-178201.
PA (SCRI) SCRIPPS RES INST.
PI Burioni R, Burton DR, Sanna PP, Williamson RA;
DP WPI: 95-264009/33.
PT Human monoclonal antibodies that neutralise Herpes simplex virus
PT (HSV) types 1 and 2 - used for diagnosis and passive immunotherapy
PT of HSV infections.
PS Disclosure: Page 72; 100pp; English.
CC R76964 is the heavy chain of the human anti-herpes monoclonal antibody
CC clone FabHSV8. This antibody is capable of neutralising both herpes
CC simplex virus (HSV) types 1 and 11 by binding an epitope present on
CC glycoprotein D. The antibody may be used for detecting HSV in vivo or
CC in vitro; for passive immunotherapy (pref. prophylactically) of HSV
CC infection (eg. genital, oral or ocular herpes), partic. as its Fab
CC fragment and as a competitive reagent for detecting neutralising
CC anti-HSV antibodies in a sample. Anti-idiotypic antibodies raised
CC against the mAb can be used for active immunotherapy of HSV infection.

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SQ Sequence 122 AA:
Query Match 60.7%; Score 565; DB 14; Length 122;
Best Local Similarity 66.7%; Pred. No. 1.41e-34;
Matches 92; Conservative 14; Mismatches 26; Indels 1; Gaps 1;

Db 1 leqsaevkkgssvkvsckasgssfsyalwvrgqggqlwmgglmpifgtayqk 60
QY 5 LQSGAEVKKPGSSVKVSQCQVGFDTFSYTIQWLPQAPGQGPWMGNIPVYNTPNYNAQK 64
Db 61 fadrlitadkststamylslsrdstavyycar--ggg-ryd-a--fdixqggltvtss 119
QY 55 EGGPSITADSTSTAYMELSLSPEDTAVYFCARVVPNAIPHTMGTMYFYDYWGQGLT 124
Db 120 *as 122
QY 125 VSS 127

RESULT 14
ID R77615 standard; Protein: 249 AA.
AC R77615:
DT 02-APR-1996 (first entry)
DE Humanised 5G1.1 VH + IGHRD.
KW Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR.
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1 19
FT /label= sig_peptide
FT Peptide 20..249
FT /label= mat_peptide
FT PN W0952697-A1.
PD 09-NOV-1995.
PF 01-MAY-1995; U05688.
PR 02-MAY-1994; US-236208.
PA (ALEX-) ALEXION PHARM INC
PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
DR WPI: 95-392923/50.
N-PSDB: T08487.
PT Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
PS Claim 37: Pages 135-137; 181pp; English.
CC A DNA construct (T08487) codes for a humanised CDR-grafted
CC light chain, designated 5G1.1 VL + IGHRD (R77615), which includes
CC CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The
CC DNA can be subcloned together with DNA (T08484) coding
CC for a humanised Fd (R77611) into vector APEX-3P (T08476) for
CC expression of humanised antibody in human 293 EBNA cells. Such
CC recombinant antibodies retain the ability of Mab 5G1.1 to block
CC human complement C5a generation and thus to reduce glomerular
CC inflammation and kidney dysfunction associated with
CC glomerulonephritis.
SQ Sequence 249 AA:

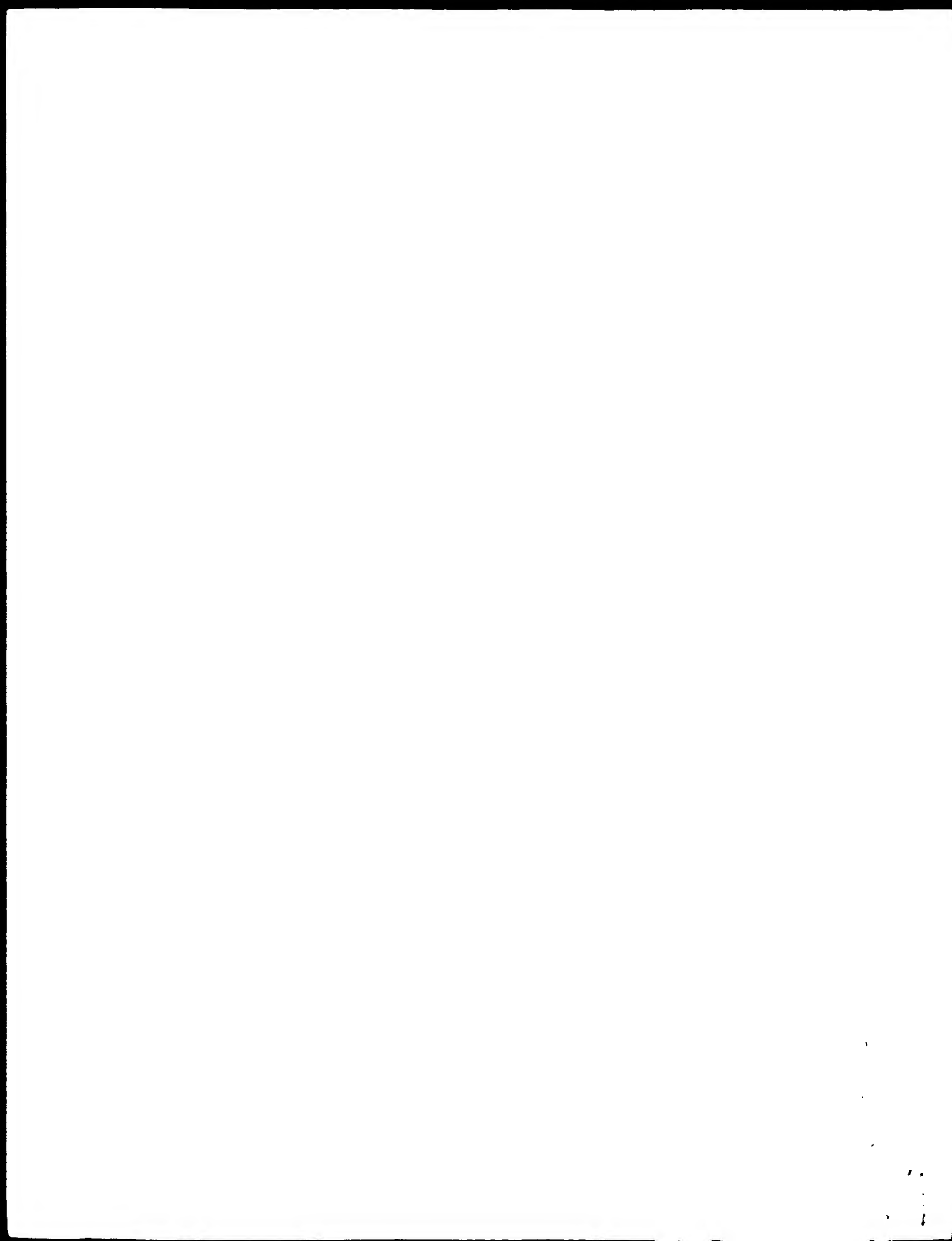
Query Match 50.3%; Score 561; DB 14; Length 249;
Best Local Similarity 66.9%; Pred. No. 2.93e-34;
Matches 85; Conservative 16; Mismatches 21; Indels 5; Gaps 3;

Db 20 qvqlv-qsgaevkkgssvkvsckasgssfsyalwvrgqggqlwmgglmpifgtayqk 78
QY 1 EVQLLEQSGARVKPKGSSVKVSQCQVGFDTFSYTIQWLPQAPGQGPWMGNIPVYNTPN 60
Db 79 yaqkfqrvtmtrdststamylslsrdstavyycar--pn---wyfdwvqg 134
QY 61 YAQKFGQGLSITADSTSTAYMELSLSPEDTAVYFCARVVPNAIPHTMGTMYFYDYWGQ 120
Db 135 tlvtvss 141
QY 121 TLIVVSS 127

Query Match 59.9%; Score 558; DB 23; Length 119;
Best Local Similarity 71.7%; Pred. No. 5.06e-34;
Matches 86; Conservative 11; Mismatches 16; Indels 7; Gaps 4;

Db 7 gglevkkgssvkvsckasgssfsyalwvrgqggqlwmgglmpifgtayqkfgg 66
QY 8 SCAEVKKPGSSVKVSQCQVGFDTFSYTIQWLPQAPGQGPWMGNIPVYNTPNYNAQKFG 67
Db 67 rvtitadkststamylslsrdstavyycar--ggg-ryd-a--fdixqggltvtvss 119
QY 68 RUSITADSTSTAYMELSLSPEDTAVYFCARVVPNAIPHTMGTMYFYDYWGQGLTIVVSS 127

Search completed: Tue Feb 24 07:06:25 1998
Job time : 33 secs.
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W W E R L D

(TM)

Release 2.1D John F. Collins, BioComputing Research Unit.
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Distribution rights by IntelliGenetics, Inc.

Mpsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on. Tue Feb 24 13:29:24 1998; MasPar time 129.01 seconds

Tabular output not generated. 805,290 Million cell updates/sec

Title: >US-08-844-215-27
Description: (1-378) from US08844215.seq
Perfect Score: 378
N.A. Sequence: 1 GAGGTGGAGTGGTGGAGTGC
Comp: CTCACGTCGACGAGCTGAG... GAGACAGTGGACAGAGT

Scoring table. TABLE default

Gap 5

Nmatch STD DBase 5 Query 0

Searched: 397346 seqs, 1410104 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: EST-C
1. EST197 2:EST128 2:EST129 4:EST130 5:EST131 6:EST132
7:EST133 8:EST134 9:EST135 10:EST136 11:EST137 12:EST138
13:EST139 14:EST140 15:EST141 16:EST142 17:EST143
18:EST144 19:EST145 20:EST146 21:EST147 22:EST148
23:EST149 24:EST150 25:EST151 26:EST152 27:EST153
28:EST154 29:EST155 30:EST156 31:EST157 32:EST158
33:EST159 34:EST160 35:EST161 36:EST162 37:EST163
38:EST164 39:EST165 40:EST166 41:EST167 42:EST168
43:EST169 44:EST170 45:EST171 46:EST172 47:EST173
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53:EST179 54:EST180 55:EST181 56:EST182 57:EST183
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83:EST209 84:EST210 85:EST211 86:EST212 87:EST213
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93:EST219 94:EST220 95:EST221 96:EST222 97:EST223
98:EST224

Database: EST-D
99:EST225 100:EST226 101:EST227 102:EST228 103:EST229
104:EST230 105:EST231 106:EST232 107:EST233 108:EST234
109:EST235 110:EST236 111:EST237 112:EST238 113:EST239
114:EST240 115:EST241 116:EST242 117:EST243 118:EST244
119:EST245

Statistics: Mean 9.914; Variance 1.852; scale 5 354
pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	132	24.3	372 99	AA221281	144902 r1 Soares ova	2 25e-21
2	119	31.5	279 26	AA300571	EST13661 Testis tumor	1 73e-193
3	111	29.4	291 58	AA377074	EST89603 Small intest	1 85e-176
4	87	23.0	265 58	AA377128	EST89660 Small intest	3 75e-126
5	78	20.6	266 00	AA402547	2047007 r1 Soares ova	1 09e-107
6	57	15.1	258 82	AA383972	EST97425 Thymus 11 Ho	6 23e-66
7	45	11.9	230 95	AA428970	144902 r1 Soares ova	2 37e-43
8	44	11.6	258 52	AA360195	EST69374 Lymph node I	1 56e-41
9	43	11.4	273 28	AA300982	EST13989 Testis tumor	1 01e-39
10	43	11.4	273 28	AA300982	EST13989 Testis tumor	1 01e-39
11	33	10.3	240 32	AA360239	EST69374 Lymph node I	1 08e-32
12	38	10.1	280 37	AA366955	EST30467 Colon I Homo	7 07e-31
13	37	9.8	294 31	AA314630	EST18648 Lung Homo sa	3 76e-29
14	35	9.3	366 59	AA378312	EST91017 Synovial sar	9 49e-26
15	34	9.0	278 60	AA381086	EST94138 Activated T-	4 49e-24
16	33	8.7	256 26	AA300600	EST13453 Testis tumor	2 03e-22
17	29	7.7	304 26	AA300945	EST13823 Testis tumor	5 14e-16
18	28	7.4	326 27	AA377241	EST30532 Colon I Homo	1 78e-14
19	24	6.2	458 22	AA145478	EST59377 r1 Soares mou	1 27e-08
20	23	6.1	439 22	AA311039	EST14427 Testis tumor	3 01e-07
21	23	6.1	364 16	AA088195	EST69374 Lymph node I	1 08e-32
22	22	5.8	371 37	AA377555	EST30921 Colon I Homo	6 49e-06
23	22	5.8	493 1	AA178135	EST13949 Testis tumor	1 26e-04
24	21	5.6	170 26	AA300909	EST59377 r1 Soares mou	1 27e-08
25	21	5.6	239 52	AA360196	EST59375 Lymph node I	1 26e-04
26	21	5.6	307 58	AA377311	EST89659 Small intest	1 26e-04
27	21	5.6	370 24	AA295093	EST100400 Pancreas tu	1 26e-04
28	21	5.6	420 1	AA175690	EST44502 r1 Soares mou	1 26e-04
29	20	5.3	253 25	AA295941	EST101165 Thymus III	2 19e-03
30	20	5.3	270 49	AA286658	EST69374 Lymph node I	1 08e-32
31	20	5.3	257 37	AA377407	EST30532 Colon I Homo	1 78e-14
32	20	5.3	288 9	AA078242	EST69374 Lymph node I	1 08e-32
33	20	5.3	298 104	HUM091A09B	Human fetal brain cDN	2 19e-03
34	20	5.3	355 51	AA357232	EST66193 LNCAP cells	2 19e-03
35	20	5.3	374 87	AA434194	EST27412 s1 Soares ova	2 19e-03
36	20	5.3	307 23	AA370880	EST69374 Lymph node I	1 08e-32
37	20	5.3	401 6	AA219325	EST17410 s1 Stratagene	2 19e-03
38	20	5.3	419 84	AA433157	EST69374 Lymph node I	1 08e-32
39	20	5.3	437 29	AA308611	EST179424 HCC cell l1	2 19e-03
40	20	5.3	441 94	AA156694	EST69374 Lymph node I	1 08e-32
41	20	5.3	587 44	AA263229	EST69374 Lymph node I	1 08e-32
42	19	5.0	249 94	AA437913	EST23400 s1 Knowles So	3 36e-02
43	19	5.0	370 24	AA295542	EST100711 Pancreas tu	2 36e-02
44	19	5.0	447 7	AA222800	EST77711 r1 Soares mou	3 36e-02
45	19	5.0	446 34	AA255640	EST2104 r1 Soares mou	3 36e-02

ALIGNMENTS

RESULT 1 AA291381 379 bp mpna EST 16-MAY-1997
144902 r1 Soares ova 100% match 100% match 100% match 100% match
6% similar to gb:U85112 IG HEAVY CHAIN HEPATOSAR V-1 REGION
(HUMAN).
ACCESSION AA291381
NID Q1939359
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Fukuyama, T., et al. 1997. Human fetal liver cDNA library. Chordata:
Vertebrata; Mammalia; Eutheria; Primates, Catarrhini; Homiidae;
Homo.
REFERENCE 1 (bases 1 to 379)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Schellenger, K., Stepien, M., Tan, F., Theisling, B.,
White, Y., Wyllie, T., Waterston, P. and Wilson, P.
TITLE WashU-Merck EST Project 1997

ORGANISM Homo sapiens
 -Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominiidae;
 Homo.

REFERENCE 1 (bases 1 to 291)
 AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, P.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, P.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, P.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudke, D.M., Shirley, P., Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.T., Dimke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

TITLE Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
 MEDLINE 95026280
 COMMENT Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the tigr Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES
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 Matches 163; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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 QY 54 TGCAAGTCTCTGAGGACAGTTCACAGCTACAAATTCATTTGAGTGGACAGGCCCC 123
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 Db 195 ggcagaggaactgaatgagtgatgaatgaacccagcaaatggaggtccgactgtgca 254
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 Db 255 cagaattttcggagagagtcacccctcaccacagac 290
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RESULT 4
 LOCUS AA377128 265 bp mRNA EST 21-APR-1997
 DEFINITION EST89660 Small intestine I Homo sapiens cDNA 5' end similar to

similar to immunoglobulin heavy chain, VDJ region.

AA377128
 g2029456
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominiidae;
 Homo.

REFERENCE 1 (bases 1 to 265)
 AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, P.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, P.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, P.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudke, D.M., Shirley, P., Small, K.V., Spriggs, T.A., Utterback, T.P., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.T., Dimke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.

TITLE Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
 MEDLINE 95026280
 COMMENT Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the tigr Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES
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 /note="Organ: small intestine; Vector: pBluescript SK-"
 Site_1: EcoRI; Site_2: XhoI
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 /dev_stage="adult"
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 Best Local Similarity 77.8%; Pred. No 3.75e-126,
 Matches 119; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Db 96 aggtcagctagtacagctctgaggtgaagtgaaagagcctgaggtcaggtcaggtct 155
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 QY 2 AGGTGCACTGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 61
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 Db 156 ctggaagagantctggtttacaccttaccacatcaggtatcagctgaggtgagcagagcc 215
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 QY 62 CTGTCAGGAGGCTCTGAGAGGAGCTTTCATCAAGCTACAAATTCATTTGAGTGG 121
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 Db 216 ctggacaaggctcaggtcaggtgaggtgatgatca 248
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 QY 122 CTGGACAAGGCTCTGAGTGGATGGAGGATCA 154
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RESULT 12

LOCUS	AA326955	280 bp	mpna	EST	20-APR-1997
DEFINITION	EST70467 Colton I Homo sapiens cDNA 5' end similar to immunoglobulin mu heavy chain, VDJC regions.				
ACCESSION	AA326955				
NID	g1979434				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryotes, mitochondrial eukaryotes, Metazoa, Chordata.				
	Vertebrata; Mammalia; Eutheria; Primates, Catarrhini, Hominoidea, Hominidae, Homo.				
REFERENCE	1 (bases 1 to 280)				
AUTHORS	Adams,M.D., Kerlavage,A.P., Fleischmann,P.D., Fullner,P.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.P., Coffin,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,I.L., Georhgian,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Heblum,E., Hinkley,Sr.,				

[illegible]

GCACAAGGTCT 134

204 2F MPNA EST 19-APR-1987

AA3114630 Lung Homo sapiens cDNA 5' end similar to

AA3115648 Immunoglobulin heavy chain, V region.

AA3114630

19966978

EST.

human.

Other species

Eukaryotes; Mitochondrial eukaryotes. Metazoa, Chordata:

Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea:

Homos.

1 (bases 1 to 294)

Adams,M.D., Kerlavage,A.R., Fleischman,P.D., Feldner,P.A.,

White,C.J., Lee,N.H., Kinsess,E.F., Weinstock,P.G., Gocayne,J.D.,

Saiton,G., Blake,A., Brandon,P.C., Man-Wai,C.,

Clayton,P.A., Cline,T.P., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,

Fraser,M., Gish,W.B., Gruber,C., Hannon,G.J., Hutchins,

Patel,R.D., Pritchard,W.M., Pritchard,J., Rhee,V.,

Samadpour,M., Scalet,A., Sinsch,M., Tabor,C., Tabor,T.,

Thompson,R., Venter,A., White,O., White,P., Young,R.A., Zannis-Hart,

et al. 1991

TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL	Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE	96026280
COMMENT	

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Job time : 507 secs.

